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(54) Title: **GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS USING ARRAYS OF CANDIDATE GENES**

(57) Abstract: The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences of subsequences thereof wherein the sequences of subsequences are overpressed in tumor cells, further wherein the sequences of subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1-468 or the complement thereof. The invention relates also to polynucleotide arrays useful to differentiate tumor cells from normal cells comprising combinations of selected immobilized polynucleotide sequences sets.

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GENE EXPRESSION PROFILING OF PRIMARY BREAST  
CARCINOMAS USING ARRAYS OF CANDIDATE GENES

5 This invention relates to polynucleotide analysis  
and, in particular, to polynucleotide expression profiling of  
carcinomas using arrays of candidate polynucleotides.

10 Pathologists and clinicians in charge of the  
management of breast cancer patients are facing two major  
problems, namely the extensive heterogeneity of the disease  
and the lack of factors - among conventional histological and  
clinical features - predicting with reliability the evolution  
of the disease and its sensitivity to cancer therapies.  
Breast tumors of the same apparent prognostic type vary  
widely in their responsiveness to therapy and consequent  
15 survival of the patient. New prognostic and predictive  
factors are needed to allow an individualization of therapy  
for each patient.

Great hope is currently being placed on molecular  
studies, which address the problem in a global fashion.  
20 Methods such as cytogenetics, comparative genomic  
hybridization, and whole-genome allelotyping have addressed  
the issue at the genome level. Currently, the modifications  
that take place in human tumors at the level of transcription  
can also be studied in a large, unprecedented scale, using  
25 new methods such as cDNA arrays that allow quantitative  
measurement of the mRNA expression levels of many genes  
simultaneously. Thus, it would be advantageous to provide a  
means to assess the capacity of cDNA array testing in  
clinical practice to better classify an heterogeneous cancer  
30 into tumor subtypes with more homogeneous clinical outcomes,  
and to identify new potential prognostic factors and  
therapeutics targets.

The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences or subsequences thereof wherein the sequences or subsequences are either underexpressed or overexpressed in tumor cells, further wherein the sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 468 or the complement thereof.

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples.

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma.

Fig. 3 is prognostic classification of breast cancer by gene expression profiling.

Fig. 4 shows the correlation of GATA3 expression with ER phenotype.

In the context of this disclosure, a number of terms shall be utilized.

The term "polynucleotide" refers to a polymer of RNA or DNA that is single-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. A polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

The term "subsequence" refers to a sequence of nucleic acids that comprises a part of a longer sequence of nucleic acids.

The term "immobilized on a support" means bound directly or indirectly thereto including attachment by

covalent binding, hydrogen bonding, ionic interaction, hydrophobic interaction or otherwise.

Breast cancer is characterized by an important histoclinical heterogeneity that currently hampers the selection of the most appropriate treatment for each case. This problem could be solved by the identification of new parameters that better predict the natural history of the disease and its sensitivity to treatment. An important object of the present invention relates to a large-scale molecular characterization of breast cancer that could help in prediction, prognosis and cancer treatment.

An important aspect of the invention relates to the use of cDNA arrays, which allows to quantitative study mRNA expression levels of 188 candidate genes in 34 consecutive primary breast carcinomas along three directions: comparison of tumor samples, correlations of molecular data with conventional histoclinical prognostic features and gene correlations. The experimentation evidenced extensive heterogeneity of breast tumors at the transcriptional level. Hierarchical clustering algorithm identified two molecularly distinct subgroups of tumors characterized by a different clinical outcome after chemotherapy. This outcome could not have been predicted by the commonly used histoclinical parameters. No correlation was found with the age of patients, tumor size, histological type and grade. However, expression of genes was differential in tumors with lymph node metastasis and according to the estrogen receptor status; ERBB2 expression was strongly correlated with the lymph node status ( $p \leq 0.0001$ ) and that of GATA3 with the presence of estrogen receptors ( $p \leq 0.001$ ). Thus, experimental results identified new ways to group tumors according to outcome and new potential targets of carcinogenesis. They show that the systematic use of cDNA



array testing holds great promise to improve the classification of breast cancer in terms of prognosis and chemosensitivity and to provide new potential therapeutic targets.

5 DNA arrays consist of large numbers of DNA molecules spotted in a systematic order on a solid support or substrate such as a nylon membrane, glass slide, glass beads or a silicon chip. Depending on the size of each DNA spot on the array, DNA arrays can be categorized as microarrays (each  
10 DNA spot has a diameter less than 250 microns) and macroarrays (spot diameter is greater than 300 microns). When the solid substrate used is small in size, arrays are also referred to as DNA chips. Depending on the spotting technique used, the number of spots on a glass microarray can  
15 range from hundreds to thousands.

DNA microarrays have serve a variety of purposes, including, gene expression profiling, de novo gene sequencing, gene mutation analysis, gene mapping and genotyping. cDNA microarrays are printed with distinct cDNA  
20 clones isolated from cDNA libraries. Therefore, each spot represents an expressed gene, since it is derived from a distinct mRNA.

Typically, a method of monitoring gene expression involves providing (1) providing a pool of sample  
25 polynucleotides comprising RNA transcript(s) of one or more target gene(s) or nucleic acids derived from the RNA transcript(s); (2) reacting, such as hybridizing the sample polynucleotide to an array of probes (for example, polynucleotides obtained from a polynucleotide library)  
30 (including control probes) and (3) detecting the reacted/hybridized polynucleotides. Detection can also involve calculating/quantifying a relative expression (transcription) level.

The present invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 in annex or the complement thereof.

Obviously, sequences having a great degree of homology with the above sequences could also been used to realize the molecular characterization of the invention, namely when those sequences present one or a few punctual mutations when compared with anyone of sequences SEQ ID Nos: 1 - 468.

The invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 249 (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex ) or the complement thereof

Preferably the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 247 (Here, these SEQ ID N° refer to old SEQ ID N° 1-247 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application

in annex); further wherein said sequences are useful in differentiating a normal cell from a cancer cell.

5 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 242 (Here, these SEQ ID N° refer to old SEQ ID N° 1-242 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex);  
10 wherein said sequences are useful in detecting a hormone sensitive tumor cell, or wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

15 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 224; (Here, these SEQ ID N° refer to old SEQ ID N° 1-224 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex)  
20 wherein said sequences are useful in differentiating tetracycline-sensitive tumors from tetracycline-insensitive tumors.

25 The invention relates also to any polynucleotide library as previously described wherein said polynucleotides are immobilized on a solid support in order to form a polynucleotide array.

30 Preferably the support is selected from the group consisting of a nylon membrane, glass slide, glass beads, or a silicon chip.

The invention concerns also a method for detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

- a) obtaining a polynucleotide sample from a patient; and
- 5        b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously described or an expression product encoded by any of the polynucleotide sequences of said
- 10        libraries and
- c) detecting the reaction product of step (b).

The invention relates also to a such method for detecting differentially expressed polynucleotide sequences

15        of the invention wherein the amount of reaction product of step (c) is compared to a control sample.

Preferably the polynucleotide sample isolated for, the sample is RNA or mRNA.

Preferably the polynucleotide sample is cDNA obtained by

20        reverse transcription of the mRNA.

In a preferred embodiment the method for detecting differentially expressed polynucleotide sequences, the step (b) comprises a hybridization of the sample RNA with the labeled probe.

25        The method for detecting differentially expressed polynucleotide sequences is used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and namely breast cancer.

30        The method for detecting differentially expressed polynucleotide sequences is particularly useful wherein the product encoded by any of the polynucleotide sequences or

subsequences is involved in a receptor-ligand reaction on which detection is based.

The invention relates also to a method for screening an anti-tumor agent comprising the method for detecting differentially expressed polynucleotide sequences previously described wherein the sample has been treated with the anti-tumor agent to be screened.

The label used to label polynucleotide samples is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent label.

The invention also relates to a library of polynucleotides comprising a population of polynucleotide sequences overexpressed or underexpresses in cells derived from a tumor selected from SEQ ID NO :1 to SEQ ID NO :249 and their respective complements. (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex).

In a particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 52 ; SEQ ID No : 54 ; SEQ ID No : 63 ; SEQ ID No : 64 ; SEQ ID No : 81 ; SEQ ID No : 82 ; SEQ ID No : 87 ; SEQ ID No : 88 ; SEQ ID No : 101 ; SEQ ID No : 102 ; SEQ ID No : 103 ; SEQ ID No : 104 ; SEQ ID No : 105 ; SEQ ID No : 107 ; SEQ ID No : 113 ; SEQ ID No : 114 ; SEQ ID No : 115 ; SEQ ID No : 116 ; SEQ ID No : 127 ; SEQ ID No : 128 ; SEQ ID No : 131 ; SEQ ID No : 139 ; SEQ ID No : 140 ; SEQ ID No : 142 ; SEQ ID No : 150 ; SEQ ID No : 151 ; SEQ ID No : 154 ; SEQ ID No : 156 ; SEQ ID

No : 160 ; SEQ ID No : 161 ; SEQ ID No : 162 ; SEQ ID No : 177 ;  
SEQ ID No : 178 ; SEQ ID No : 194 ; SEQ ID No : 195 ; SEQ ID No :  
227 ; SEQ ID No : 228 ; SEQ ID No : 229 ; SEQ ID No : 231 ; SEQ ID  
No : 233 ; SEQ ID No : 243 ; SEQ ID No : 244 ; SEQ ID No : 245 ;  
5 SEQ ID No : 246 ; SEQ ID No : 247, (Here, these SEQ ID N° refer  
to old SEQ ID N° presented on table 5 in priority document,  
the correlation table 10 allows to identify these sequences  
in the sequence listing of the present application in annex),  
which distinguish a healthy person from a person with cancer.

10 Preferably the invention relates to  
polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID  
No : 102 ; SEQ ID No : 103 ; SEQ ID No : 107 ; SEQ ID No : 229 ;  
SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 243 ; SEQ ID No :  
244 ; SEQ ID No : 245 ; SEQ ID No : 246 ; SEQ ID No : 247 (Here,  
15 these SEQ ID N° refer to old SEQ ID N° presented on table 6  
in priority document, the correlation table 10 allows to  
identify these sequences in the sequence listing of the  
present application in annex), which distinguish a healthy  
person from a person with cancer.

20 In another particular embodiment the invention relates  
to polynucleotide sequences: SEQ ID No : 2 ; SEQ ID No : 3 ;  
SEQ ID No : 4 ; SEQ ID No : 5 ; SEQ ID No : 6 ; SEQ ID No : 7 ;  
SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 10 ; SEQ ID No : 11 ;  
25 SEQ ID No : 12 ; SEQ ID No : 13 ; SEQ ID No : 14 ; SEQ ID No : 15  
; SEQ ID No : 16 ; SEQ ID No : 17 ; SEQ ID No : 18 ; SEQ ID No :  
19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No  
: 23 ; ; SEQ ID No : 24 ; SEQ ID No : 25 ; SEQ ID No : 26 ; SEQ ID  
No : 27 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 223 ;  
30 SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer  
to old SEQ ID N° presented on table 7 in priority document,  
the correlation table 10 allows to identify these sequences  
in the sequence listing of the present application in annex)  
which detect hormone sensitive tumors.

Preferably the invention relates to polynucleotide sequences SEQ ID No : 1; SEQ ID No : 2 SEQ ID No : 3; SEQ ID No : 4; SEQ ID No : 5; SEQ ID No : 221; SEQ ID No : 222 ; SEQ ID No : 15; SEQ ID No : 16; SEQ ID No : 17; SEQ ID No : 18 ; SEQ ID No : 19; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 241; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which detect hormone sensitive tumors.

In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 3 ; SEQ ID No : 4 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 23 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 33 ; SEQ ID No : 34 ; SEQ ID No : 35 ; SEQ ID No : 36; SEQ ID No : 37; SEQ ID No : 38; SEQ ID No : 39; SEQ ID No : 40 ; SEQ ID No : 41 ; SEQ ID No : 42 ; SEQ ID No : 43 ; SEQ ID No : 44 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 233 ; SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

Preferably the invention relates to polynucleotide sequences : SEQ ID No : 1 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No : 28; ; SEQ ID No : 29 ; SEQ ID No : 29 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 37 ; SEQ ID No : 38 ; SEQ ID No : 39 ; SEQ ID No : 241 ; SEQ ID No : 241, (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to

identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

5           In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 2 ;  
SEQ ID No : 6 ; SEQ ID No : 7 ; SEQ ID No : 8 ; SEQ ID No : 9 ;  
SEQ ID No : 10 ; SEQ ID No : 11 ; SEQ ID No : 13 ; SEQ ID No : 14  
10       ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No :  
22 ; SEQ ID No : 23 ; SEQ ID No : 35 ; SEQ ID No : 36 ; ; SEQ ID  
No : 37 ; SEQ ID No : 56 ; SEQ ID No : 57 ; SEQ ID No : 74 ; SEQ  
ID No : 75 ; SEQ ID No : 102 ; SEQ ID No : 104 ; SEQ ID No : 107  
; SEQ ID No : 108 ; SEQ ID No : 109 ; SEQ ID No : 118 ; SEQ ID No  
: 119 ; ; SEQ ID No : 136 ; SEQ ID No : 213 ; SEQ ID No : 214 ;  
15       SEQ ID No : 215 ; SEQ ID No : 223 ; SEQ ID No : 224 (Here, these  
SEQ ID N° refer to old SEQ ID N° presented on table 11 in  
priority document, the correlation table 10 allows to  
identify these sequences in the sequence listing of the  
present application in annex) which distinguish tumors  
20       sensitive to anthracycline from tumors unsensitive to  
anthracycline.

          The invention relates also to a method of detecting  
differentially expressed genes correlated with a cancer  
25       comprising detecting at least one library of polynucleotide  
sequences as above defined or of products encoded by said  
library in a sample obtained from a patient.

          A particular embodiment of the invention relates  
30       to a polynucleotide library of corresponding substantially to  
any combination of at least one polynucleotide sequence  
selected among those included in each one of predefined  
polynucleotide sequences sets 1 to set 212 as defined in  
table 4



The invention relates obviously to polynucleotide libraries comprising at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of said predefined sets, allowing to obtain a discriminating gene pattern, namely to distinguish between normal patients and patients suffering from tumor pathology, between patients having an hormone sensitive tumor and patients having an hormone resistant tumor, between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes, between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor and between patients having good prognosis primary breast tumors and patients having poor prognosis primary breast tumors.

Polynucleotide sequences library useful for the realization of the invention can comprise also any sequence comprised between 3'end and 5'end of each polynucleotide sequence set as defined in table 4, allowing the complete detection of the implicated genes.

The invention relates also to a polynucleotide library useful to differentiate a normal cell from a cancer cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

Preferably the polynucleotide library useful to differentiate a normal cell from a cancer cell correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated in table 5B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 5A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 5B allows to distinguish between normal patients, and patients suffering from tumor pathology.

The invention relates also to a polynucleotide library useful to detect a hormone sensitive tumor cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

Preferably the polynucleotide library useful to detect a hormone sensitive tumor cell correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 6A, together with detection of an underexpression of

genes identified with sets of polynucleotides sequences defined in table 6B allows to distinguish between patients having an hormone sensitive tumor and patients having an hormone resistant tumor.

5

The invention concerns also a polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 7A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 7B allows to distinguish between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes.

The invention concerns also a polynucleotide library useful to differentiate anthracycline-sensitive tumors

from anthracycline-insensitive tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide library useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 8A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 8B allows to distinguish between patients having an anthracycline-sensitive tumor from patients having an anthracycline-insensitive tumor.

The invention concerns also a polynucleotide library useful to classify good and poor prognosis primary breast tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide library useful to classify good and poor prognosis primary breast tumors correspond substantially to any combination of at least one

polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 9A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 9B allows to classify patients having good and poor prognosis primary breast tumors.

In a preferred embodiment, the tumor cell presenting underexpressed or overpressed sequences from the polynucleotide library of the invention are breast tumor cells.

In a particular embodiment the polynucleotides of the polynucleotide library of the present invention are immobilized on a solid support in order to form a polynucleotide array, and said solid support is selected from the group consisting of a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

Another object of the present invention concerns a polynucleotide array useful for prognosis or diagnostic of tumor comprising at least one immobilized polynucleotide library set as previously defined.

Then the invention concerns a polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of at least one polynucleotide sequence selected among those included in each

one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

5 Preferably the polynucleotide array useful to differentiate a normal cell from a cancer cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each  
10 one of predefined polynucleotide sequences sets indicated in table 5B.

The invention relates also to a polynucleotide array useful to detect a hormone sensitive tumor cell  
15 comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

20 Preferably the polynucleotide array useful to detect a hormone sensitive tumor cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in  
25 table 6B.

The invention concerns also a polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of at  
30 least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The invention concerns also a polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The invention concerns also a polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide array useful to classify good and poor prognosis primary breast tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The present invention concerns also a method for detecting differentially expressed polynucleotide sequences that are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient; and

b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously defined or an expression product encoded by any of the polynucleotide sequences of the libraries previously defined

c) detecting the reaction product of step (b).

Preferably, the polynucleotide sample obtained at step (a) is labeled before its reaction at step (b) with the probe immobilized on a solid support.

The label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.



In a particular embodiment the reaction product of step (c ) is quantified by further comparison of said reaction product to a control sample.

5 In a first embodiment, the polynucleotide sample isolated from the patient and obtained at step (a) is either RNA or mRNA.

In another embodiment the polynucleotide sample isolated from the patient is cDNA is obtained by reverse transcription of the mRNA.

10 Preferably the reaction step (b) of the method for detecting differentially expressed polynucleotide sequences comprises a hybridization of the sample RNA issued from patient with the probe.

15 Preferably the sample RNA is labeled before hybridization with the probe and the label is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

20 This method for detecting differentially expressed polynucleotide sequences is particularly useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and particularly breast cancer.

25 The method for detecting differentially expressed polynucleotide sequences is also particularly useful when the product encoded by any of the polynucleotide sequences or subsequences set is involved in a receptor-ligand reaction on which detection is based.

30 The present invention is also related with a method for screening an anti-tumor agent comprising the method the above-depicted method for detecting differentially expressed polynucleotide sequences wherein the sample has been treated with the anti-tumor agent to be screened.

In a particular embodiment the method for screening an anti-tumor agent comprises detecting polynucleotide sequences reacting with at least one library of polynucleotides or polynucleotide sequences set as previously defined or of products encoded by said library in a sample obtained from a patient.

The invention is illustrated by examples detailed below related to particular experimental results obtained with selected libraries of polypeptides useful to identify and distinguish tumor samples from normal ones.

#### Tumor samples and RNA extraction

To avoid any bias of selection as to the type and size of the tumors, the RNAs to be tested were prepared from unselected samples. Samples of primary invasive breast carcinomas were collected from 34 patients undergoing surgery at the Institute Paoli-Calmette. After surgical resection, the tumors were macrodissected: a section was taken for the pathologist's diagnosis and an adjacent piece was quickly frozen in liquid nitrogen for molecular analyses. The median age of patients at the time of diagnosis was 55 years (range 39, 83) and most of them were post-menopausal. Tumors were classified according to the WHO histological typing of breast tumors in: 29 ductal carcinomas, 2 lobular carcinomas, 1 mixed ductal and lobular carcinoma, and 2 medullar carcinomas. They had various sizes, inferior or equal to 20 mm (n = 13), between 20 and 50 mm (n = 18) or superior to 50 mm (n = 3), axillary's lymph node status (negative: 19 tumors, positive: 15 tumors), SBR grading (I: 3 tumors, II: 20 tumors, III: 10 tumors, not evaluable: 1 tumor), and estrogen receptor status (ER) evaluated by

immunohistochemical assay (23 ER-positive, 11 ER-negative). ER positivity cutoff value was 10%. Adjuvant treatment with radiotherapy and when necessary multi-agent anthracyclin-based chemotherapy (n = 16) was given to patients according to local practice.

Total RNA was extracted from tumor samples by standard methods (43). Total RNA from normal breast tissue was obtained from Clontech (Palo Alto, CA): RNA was isolated from 8 tissue specimens from Caucasian females, age range 23 - 47. RNA integrity was controlled by denaturing formaldehyde agarose gel electrophoresis and Northern blots using a 28S-specific oligonucleotide.

#### cDNA arrays preparation

Gene expression was analyzed by hybridization of arrays with radioactive probes. The arrays contained PCR products of 5 control clones, and 180 IMAGE human cDNA clones selected with practical criteria (3' sequence of mRNA, same cloning vector, host bacteria and insert size). This represented 176 genes (4 genes were represented by 2 different clones): 121 with proven or putative implication in cancer and 55 implicated in immune reactions (the list is available on the web site: <http://tagc.univ-mrs.fr/pub/Cancer/>). Their identity was verified by 5' tag-sequencing of plasmid DNA and comparison with sequences in the EST (dbEST) and nucleotide (GenBank) databases at the NCBI. Identity was confirmed for all but 14 clones without significant gene similarity, which were referenced by their GenBank accession number. The control clones were: Arabidopsis thaliana cytochrome c554 gene (used for hybridization signal normalization), 3 poly(A) sequences of different sizes and the vector pT7T3D (negative controls).

PCR amplification, purification and robotical spotting of PCR products onto Hybond-N+ membranes (Amersham) were done according to described protocols (4). All PCR products were spotted in duplicate. For normalization purpose, the c554 gene was spotted 96-fold scattered over the whole membrane.

#### cDNA array hybridizations

Hybridizations were done successively with a vector oligonucleotide (to precisely determine the amount of target DNA accessible to hybridization in each spot), then after stripping of vector probe, with complex probes made from the RNAs (4). Each complex probe was hybridized to a distinct filter. Probes were prepared from total RNA with an excess of oligo(dT25) to saturate the poly(A) tails of the messengers, and to insure that the reverse transcribed product did not contain long poly(T) sequences. A precise amount of c554 mRNA was added to the total RNA before labeling to allow normalization of the data.

Five ng of total RNA (~100ng of mRNA) from tissue samples were used for each labeling. Probe preparation and hybridization of the membranes were done according to known procedures (<http://tagc.univ-mrs.fr/pub/Cancer/>).

Hybridization was done in excess of target (~15 ng of DNA in each spot) and binding of cDNAs to the targets was linear and proportional to the quantity of cDNA in the probe.

#### Detection and quantification of cDNA array hybridization signals

Quantitative data were obtained using an imaging plate device. Hybridization signal detection with a FUJI BAS 1500 machine and quantification with the HDG Analyzer

software (Genomic Solutions, Ann Arbor, MI) were done as previously described (<http://tagc.univ-mrs.fr/pub/Cancer/>). Quantification was done by integrating all spot pixel intensities and subtracting a spot background value determined in the neighboring area. Spots were located with a Laplacian transformation. Spot background level was the median intensity of all the pixels present in a small window centered on the spot and which were not part of any spot (44). Quantified data were normalized in three steps and expressed as absolute gene expression levels (i.e. in percentage of abundance of individual mRNA with respect to mRNA within the sample), as described (4).

#### Array data analysis

Before analysis of the results, the reproducibility of the experiments was verified by comparing duplicate spots, or one hybridization with the same probe on two independent arrays, or two independent hybridizations with probes prepared from the same RNA. In every case, the results showed good reproducibility with respective correlation coefficients of 0.95, 0.98 and 0.98 (data not shown). Moreover, genes represented by two different clones on the array, such as CDK4 or ETV5, displayed similar expression profiles for the two clones in all samples. This reproducibility was sufficient enough to consider a 2-fold expression difference as significantly differential.

For graphical representation, data were displayed as absolute expression levels (Fig. 2a). For better visualization of clustering, results were log-transformed and displayed as relative values median-centered in each row and in each column (Fig. 2b). Hierarchical clustering was applied to the tissue samples and the genes using the Cluster program developed by Eisen (45) (average linkage clustering

using Pearson correlation as similarity metric). Results in Figs. 2 and 3 were displayed with the TreeView program (45).

Subsequent analysis was done using Excel software (Microsoft) and statistical analyses with the SPSS software. Metastasis-free survival and overall survival were measured from diagnosis until the first metastatic relapse or death respectively. They were estimated with the Kaplan-Meier method and compared between groups with the Log-Rank test. Correlations of gene pairs based on expression profiles were measured with the correlation coefficient  $r$ . The search for genes with expression levels correlated with tumor parameters was done in several successive steps.

First, genes were detected by comparing their median expression level in the two subgroups of tumors discordant according to the parameter of interest. The median values rather than the mean values were used because of the high variability of the expression levels for many genes, resulting in a standard deviation of expression level similar or superior to the mean value and making comparisons with means impossible. Second, these detected genes were inspected visually on graphics, and finally, an appropriate statistical analysis was applied to those that were convincing to validate the correlation. Comparison of GATA3 expression between ER-positive tumors and ER-negative tumors was validated using a Mann-Witney test. Correlation coefficients were used to compare the gene expression levels to the number of axillary nodes involved.

#### Northern blot analysis

Seventy-nine breast tumors, including 22 of the 34 tested on the arrays, were analyzed for GATA3 expression by Northern blot hybridization. RNA extraction from tumor samples and Northern blots were done as previously described

(43). The GATA3 probe was prepared from the IMAGE cDNA clone 129757, which corresponds to the 3' region (from +843 to +1689) of the GATA3 cDNA sequence (GenBank accession no. X55122). The insert (846 bp) was obtained by digestion of the clone with EcoRI and PacI enzymes. Northern blots were stripped and re-hybridized using a  $\alpha$ -actin probe (46).

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples. Each cDNA array on Nylon filter was hybridized with a complex probe made from 5  $\mu$ g of total RNA. The top image corresponds to the whole membrane. For the two bottom images, only the right portion of the membranes is shown. Numbers below the spots indicate housekeeping genes (1, GAPDH and 2, actin), negative control clones (3, 4 and 5) and examples of genes differentially expressed between NB and breast tumor (6, stromelysin3; 7, ERBB2; 8, MYBL2; 9, FOS; 10, TGF $\beta$ 3; 11, desmin), and between ER- breast tumor and ER+ breast tumor (12, GATA3).

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma. Each column corresponds to a single tissue, and each row to a single gene. (a) The results are expressed as percentage abundance of individual mRNA within the sample, and are represented using a blue color scale. The color scale (log scale with a 3-fold interval) indicated at the bottom left ranges from light blue (expression level 0.001%) to dark blue (expression level > 3%). White squares indicate clones with undetectable expression levels and gray squares indicate missing data. The tissue samples are arbitrarily ordered and the clones are ordered from top to bottom according to increasing median expression levels. Horizontal black arrows on the right of the figure mark three clones with highly variable expression levels between the

tumors (stromelysin3, IGF2, GATA3 from top to bottom). (b) The results are shown as relative expression levels (relative to the median value of each row and each column) and are represented with a color scale indicated at the bottom left ranging from 1/100 to 100 fold changes (gray squares: missing data). Eighteen clones with median expression level equal to zero in the 34 tumors are omitted. The clustering program arranges samples ( $n = 35$ ) along the horizontal axis so that those with the most similar expression profiles are placed adjacent to each other. Similarly, clones ( $n = 162$ ) are near each other along the vertical axis if they show a strong expression profile correlation across all tissues. The length of the branches of the dendrograms capturing respectively the samples (top) and the clones (left) reflects the similarity of the related elements. Two groups of tumors are separated and color coded: group A (blue) and group B (orange). Horizontal black and horizontal red arrows on the right of the figure respectively mark three genes with highly variable expression levels between the tumors (IGF2, GATA3, stromelysin3 from top to bottom) and four pairs of different clones representing four genes. (c) Zoom representation of group A from Figure 2b, excluding the two outlier tumors at the right. The clustering separates two subgroups of tumors, A1 and A2. The dotted branches correspond to tumors associated with metastatic relapse and death. Follow-up was longer in A2 than in A1 (median 81 months vs 47 for A1).

Fig. 3 is prognostic classification of breast cancer by gene expression profiling showing that gene expression-based tumour classification correlates with clinical outcome. The 12 samples of group A (see figure 2b and 2c) were reclustered using the top 32 differentially expressed genes between A1 and A2 subgroups. Data were displayed as in Fig. 2b and shown with the same color key.



The hierarchical clustering was applied to expression data from the 23 clones, out of 32, of which expression levels presented an at least two-fold change in at least two samples (out of 12). Two subgroups of tumors A1 and A2 are shown as well as two groups of differentially expressed clones. The dotted branches of tumor cluster A1 correspond to samples associated with metastatic relapse and death. Figure 3a shows Two-dimensional representation of hierarchical clustering results shown in figures 2a and 2b. The analysis delineates 4 groups of tumours A, B, C and D. Black squares indicate patients alive at last follow-up visit and red squares indicate patients who died. Three classes of patients with a statistically different clinical outcome were defined according to gene expression profiles: class A (n = 16), class B+C (n = 34), class D (n = 5). Figure 3b illustrates Kaplan-Meier plot of overall survival of the 3 classes of patients ( $p < 0.005$ , log-rank test). And figure 3c illustrates Kaplan-Meier plot of metastasis-free survival of the 3 classes of patients ( $p < 0.05$ , log-rank test).

Fig. 4 shows the correlation of GATA3 expression with ER phenotype. (a) The expression levels of GATA3 in 34 breast cancer samples (y axis) monitored by cDNA array analysis are reported in percentage of abundance of individual mRNA with respect to mRNA within the sample (log scale). GATA3 is significantly overexpressed in the ER-positive tumors (n = 23) versus the ER-negative tumors (n = 11) using the Mann-Witney test ( $p = 0.0004$ ). The expression level of GATA3 in normal breast tissue is reported on the right (NB). (b) Northern blot analysis of GATA3 in normal breast sample (NB) and 9 breast cancer samples (AT: tumor analyzed with cDNA array and Northern blot; NT: tumor analyzed with Northern blot). Blots were probed successively

with cDNA from GATA3 (top) and  $\alpha$ -actin (bottom). ER status is indicated for each tumor sample.

#### Data representation

5 Fig. 1 shows examples of hybridizations of cDNA arrays with probes made from RNA extracted from normal breast tissue and breast tumors.

10 The crude results of all hybridizations were processed to be presented either as absolute or relative values in schematic figures. The normalization procedure allowed display of absolute values expressed in percent of abundance of mRNA in the probe as shown in Fig. 2a. Each level of the blue color ladder represents a 3-fold interval of absolute abundance of mRNA. Each column corresponds to a tissue sample and each row to a gene. For graphic purposes, genes were ordered from top to bottom according to increasing median expression levels. Tumor samples were not ordered. The values in each sample displayed a wide range of intensities (3 decades in log scale) corresponding to expression levels ranging from approximately 0.002% to 5% of mRNA abundance. Many genes (see for example stromelysin 3, IGF2 and GATA3, arrows) displayed highly variable expression levels across all tumor samples, scattered over the whole dynamic range of values. A representation of relative values is shown in Fig. 2b. Absolute values were log-transformed, omitting 18 clones whose median intensity was equal to zero across all tissues. Data for each of the 162 remaining clones were then median-centered, as well as data for each sample, so that the relative variation was shown, rather than the absolute intensity. A color scale was used to display data: red for expression level higher than the median and green for expression level lower than the median. The magnitude of the deviation from the median was represented by

15

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the color intensity. A hierarchical clustering program was then applied to group the 35 samples according to their overall gene expression profiles, and to group the 162 clones on the basis of similarity of their expression levels in all tissues. This resulted in a picture highlighting groups of correlated tissues and groups of correlated genes as depicted by dendrograms.

#### Breast tumor classification

As shown in Fig. 2b, the clustering algorithm identified two groups of samples, designated A ( $n = 15$ , including normal breast, NB) and B ( $n = 20$ ). These groups were similar with respect to patient age, menopausal status at diagnosis, SBR grading and tumor pathological size. However, 72% of tumors in group A were node-positive and 75% in group B were node-negative. Moreover, 80% of the tumors in group B were estrogen receptor (ER) positive and 50% in group A were ER-negative. With a median follow-up of 44 months after diagnosis, overall survival was different between A and B groups: 5 women died in A (median follow-up 58 months) and 1 in B (median follow-up 40 months). But the frequency of metastatic relapse was relatively similar in the two groups, with 5 women who relapsed in A and 6 in B. Because the time between the diagnosis of metastasis and last follow-up is too short in B, a longer follow-up is needed to determine if these two different groups, defined with expression profiles, have really a different outcome with respect to overall survival.

In the group A of 15 samples, three samples (normal breast and two tumors) were different from each other and from the other 12 samples. The latter constituted two subgroups of tumors, A1 ( $n = 6$ ) and A2 ( $n = 6$ ), which could be further separated by clustering as shown in Fig. 2c. The

12 tumors had an uniformly high risk of metastatic relapse according to conventional prognostic features as shown in Table 1. Most of them had received comparable adjuvant anthracyclin-based chemotherapy after surgery, with more women treated in the A1 subgroup. Interestingly, these two subgroups, which could not be distinguished with commonly used histoclinical features, had a very different clinical outcome: there were 4 metastatic relapses and 4 deaths in A1 (median follow-up: 44 months). In contrast and despite a longer median follow-up (90 months), no metastasis or death occurred in A2. This resulted in a significant better metastasis-free survival ( $p = 0.01$ ) and overall survival ( $p = 0.005$ ) for group A2 than for group A1 tumors. No such subgrouping could be done in B.

TABLE 1

Subgroup	A1												A2											
Tumor position in the cluster	1	2	3	4	5	6							7	8	9	10	11	12						
Age, years	46	58	60	63	51	58							46	47	50	47	46	66						
Nodal status	1	0	0	16	13	37							10	4	1	2	0	0						
Histological size, mm	60	20	26	35	20	30							27	25	30	25	20	22						
SBR grade																								
ER status		neg	neg	neg	neg	neg	neg						pos	neg	pos	pos	pos	pos						
Adjuvant chemotherapy		yes	yes	no	yes	yes	yes						yes	yes	no	yes	no	no						
Metastasis		yes	no	yes	yes	no	yes						no	no	no	no	no	no						
Follow-up, months	58	106	35	47	41	31							85	98	95	49	19	141						
Patient status	D	A	D	D	A	D							A	A	A	A	A	A						

Patient characteristics in subgroups A1 and A2. The 12 tumors are numbered from 1 to 12 according to their position from left to right in the clustering graphic displayed in Fig. 3. Adjuvant chemotherapy was anthracyclin-based. In the line concerning the patient status, A means alive and D means death from cancer progression.

Genes responsible for group A substructure were searched. These are potentially relevant to the prognosis and the sensitivity to chemotherapy in these tumors. Thirty-two genes out of 188 were identified by comparing their median expression level in A1 vs A2. Then, the 12 tumors were reclustered using the expression profiles of these genes as shown in Fig. 3. The same subgroups A1 and A2 were evident and separated by 2 groups of genes: as expected, high expression of ERBB2, MYC and EGFR was associated with bad prognosis subgroup A1 (6-8), and that of E-cadherin and the proto-oncogene MYB with good prognosis subgroup A2 (9, 10). For most of the other genes, these results may stimulate new investigations. Differentiation state is a good prognostic factor in breast cancer and, accordingly, genes associated with cell differentiation, such as GATA3 (11) and CRABP2 (12), had a high level of expression in the better outcome group. The high expression of Ephrin-A1 mRNA in the bad prognosis subgroup suggests a role of this growth factor in breast cancer and can be paralleled with its up-regulation during melanoma progression (13).

#### Differential gene expression between normal breast and breast tumors

To identify genes differentially expressed between breast tumors (T) and normal breast (NB), the NB value for each gene was compared to its expression level in each tumor. When the expression level of a gene in NB was undetectable, only qualitative information could be deduced and the mRNA was considered as differentially expressed if the signal intensity in the tumor was superior to the reproducibility threshold (0.002% of mRNA abundance). In the other cases, differential expression was defined by an at least 2-fold expression difference. Also, the number of

tumors where it was over- or underexpressed was measured. Table 2 shows a list of the top 20 over- and underexpressed genes. For these genes, the T/NB ratio is reported, where T represented their median expression value in the 34 tumors. This ratio ranged from 2.70 (ABCC5) to 17.76 (GATA3) for the overexpressed genes, and from 0.00 (desmin) to 0.29 (APC) for the underexpressed genes.

**TABLE 2**

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Overexpressed genes				
154343	Granzyme H	GZMH	14q11.2	32	9,51
235947	Stromelysin 3	STMY3	22q11.2	31	15,92
207378	MYB Related Protein B	MYBL2	20q13.1	31	(a)
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	1q21.3	29	7,16
129757	GATA-binding protein 3	GATA3	10p15	28	17,76
120649	T-Lymphocyte surface CD2 antigen	CD2	1p13.1	28	7,54
109677	CREB Binding Protein	CREBBP	16p13.3	28	5,08
172152	EGFR-binding protein GRB2	GRB2	17q24-q25	28	5,00
66969	Transcription factor RELB	RELB	19	28	3,61
182007	ETS-Related Transcription Factor ELF1	ELF1	13q13	27	3,58
153446	LIM domain protein RIL	RIL	5q31.1	26	4,03
203394	ETS Variant gene 5 (ETS-related molecule)	ETV5	3q28	25	3,67
160963	Thrombospondin 1	THBS1	15q15	25	3,39
188393	POU domain, class 2, transcription Factor 2	POU2F2	19	24	4,02

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
187822	Integrin, beta 2	ITGB2	21q22.3	24	3,01
243907	Nuclear Factor of Activating T cell Subunit p45	NF45	1	24	2,84
158347	EST H27202	EST		23	2,91
230933	EST AW184517	EST		22	2,85
212366	ATP-Binding Cassette, sub-family C (CFTR/MRP), 5	ABCC5	3q27	22	2,70
149401	Cathepsin D	CTSD	11p15.5	21	2,97
	Underexpressed genes				
153854	Desmin	DES	2q35	34	0,00
208717	P55-C-FOS proto-oncogene protein	FOS	14q24.3	33	0,05
159093	Transcription Factor AP4	TFAP4	16p13	33	0,11
124340	Tenascin XA	TNXA	6p21.3	33	0,14
133738	Prolactin	PRL	6p22.2-p21.3	32	0,00
133891	Chorionic Somatomammotropin Hormone 1	CSH1	17q22-q24	32	0,00
151501	Tyrosine Kinase Receptor TEK	TEK	9p21	32	0,00
183030	Activating Transcription Factor 3	ATF3	1	32	0,07
120916	Phosphodiesterase I	PDNP2	8q24.1	32	0,14
155716	EST R72075	EST		31	0,00
208118	Transforming Growth Factor Beta Receptor Type III	TGFB3	1p33-p32	31	0,14
187547	Diphtheria Toxin Receptor	DTR	5q23	31	0,17
108490	HIV-1 Rev Binding protein	HRB	2q36	31	0,20
147002	B-cell CLL/lymphoma 2	BCL2	18q21.3	31	0,26
182610	Microsomal Glutathione S Transferase 1	MGST1	12p12.3-p12.1	31	0,28
152802	Phospholipase A2 Membrane	PLA2G2A	1p35	30	0,03



Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Associated, group IIA				
183087	Interleukin 3 Receptor Alpha chain	IL3RA	Xp22.3;Yp13.3	30	0,24
108571	Retinoblastoma-Like 2 (p130)	RBL2	16q12.2	29	0,28
125294	Adenomatous Polyposis Coli Protein	APC	5q21-q22	29	0,29
151767	FASL Receptor	TNFRSF6	10q24.1	28	0,27

List of the genes that show the most frequent differential expression between normal breast tissue and 34 breast carcinomas as measured by cDNA array analysis. N indicates the number of tumor samples where the gene is dysregulated (fold change > 2) compared to normal breast tissue. T/NB represents the ratio: median expression level in 34 breast tumors / expression level in normal breast. (a) MYBL2 transcript displayed a median expression level of 0.025% in breast tumors and was undetectable in NB.

High expression of mucin 1, NM23, ERBB2, FGFR1 and FGFR2, MYC, stromelysin3, cathepsin D and downregulation of FOS, APC, RBL2, FAS, BCL2 were found, reflecting what is known about their biology in cancer. GATA3, which codes for a member of the GATA family of zinc finger transcription factors, and CRABP2, encoding one of the two cellular retinoic acid-binding proteins, showed high expression of mRNA, extending previous results on cDNA arrays (4).

Differential gene expression among various breast tumors and correlation with histoclinical prognostic parameters

To search for potential prognostic markers in breast cancer, genes with expression levels correlated with conventional histoclinical prognostic parameters were looked for: age of patients, axillary node status, tumor size, histological grade and ER status. No significant correlation was found with age, tumor size and histological grade. However, the expression profiles of some genes correlated with ER status and axillary node involvement.

To identify genes potentially relevant to the hormone-responsive phenotype, the gene expression profiles in ER-positive breast cancers (n = 23) vs ER-negative breast cancers (n = 11) were compared. Sixteen clones displayed a median intensity of 0 in both groups. Twenty-five presented a fold change superior to 2. Table 3a displays the top 10 over- and underexpressed genes. Among them, the most differentially expressed was GATA3 with a median intensity ratio ER+/ER- of 28.6 and a value for the first quartile of ER-positive tumors superior (5-fold) to the value of the third quartile of the ER-negative tumors as shown in Fig. 4a. The high expression of GATA3 in ER-positive tumors was statistically significant using a Mann-Witney test (p 0.001). All ER-positive tumors and only 18% of ER-negative tumors displayed a GATA3 expression level greatly superior (fold change > 3) to the normal breast value. Furthermore GATA3 expression was analyzed by Northern blot hybridization (Fig. 4b) in a panel of 79 breast cancers (21 ER-negative tumors and 58 ER-positive tumors), including 22 of the tumors analyzed with cDNA arrays. It confirmed the array results for those 22 tumors as well as the strong correlation between ER status and GATA3 RNA expression (Mann-Witney test, p ≤ 0.0001).

TABLE 3A

Clone ID	Gene/Protein identity	Gene symbol	ER+/ER-
129757	GATA-binding protein 3	GATA3	28,6
356763	Granzyme A	GZMA	5,7
248613	MYB proto-oncogene	MYB	3,4
211999	KIAA1075 protein	KIAA1075	3,3
235947	Stromelysin 3	STMY3	3,1
229839	Macrophage Stimulating 1	MST1	2,8
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	2,7
301950	X-box Binding Protein 1	XBP1	2,7
205314	Tumor Protein p53	TP53	2,5
126233	Insulin-like Growth Factor 2	IGF2	2,4
66322	CD3G antigen, Gamma	CD3G	0,0
195022	Interleukin 2 Receptor Gamma chain	IL2RG	0,0
111461	SOX4 Protein	SOX4	0,4
151475	Epidermal Growth Factor Receptor	EGFR	0,5
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,5
130788	Topoisomerase (DNA) II beta (180kD)	TOP2B	0,6
323948	SOX9 Protein	SOX9	0,6
183641	S100 calcium-binding protein Beta	S100B	0,6
246620	EST N53133	EST	0,6
231424	Glutathione S Transferase Pi	GSTP1	0,6

To search for genes whose expression profile was correlated with axillary lymph node status, a strong prognostic factor in breast cancer, the group of node-negative tumors (n = 19) was compared with the group of tumors with massive axillary extension (10 or more positive nodes). Furthermore, because survival decreases with the increase of the number of tumor-involved lymph nodes and because the expression measurements were quantitative, it was looked for a correlation between the expression levels of

these genes and the number of tumor-involved nodes (quantitative variables). Table 3b shows a list of the top 10 over- and underexpressed genes between these 2 groups. Most of these genes have not been previously reported as associated with node status, but some of these results are in agreement with literature data. The gene encoding the tyrosine kinase receptor ERBB2 was the most significantly overexpressed gene in node-positive tumors and displayed the highest correlation coefficient ( $r = 0.68$  ;  $p \leq 0.0001$ ).

TABLE 3B

Clone ID	Gene/Protein identity	Gene symbol	N-/10N+
129757	GATA-binding protein 3	GATA3	11,0
160963	Thrombospondin 1	THBS1	6,6
151475	Epidermal Growth Factor Receptor	EGFR	5,4
120916	Phosphodiesterase I	PDNP2	4,9
183030	Activating Transcription Factor 3	ATF3	4,6
211999	KIAA1075 protein	KIAA1075	4,5
110480	Nuclear Factor 1 A-type	NF1A	4,5
182264	P-Selectin	SELP	4,4
356763	Granzyme A	GZMA	4,3
214008	E-cadherin	CDH1	4,0
147016	ERBB2 Receptor Protein-Tyrosine Kinase	ERBB2	0,2
179197	Protein Phosphatase PP2A, 55 kD Subunit	PP2A BR gamma	0,2
231424	Glutathione S Transferase Pi	GSTP1	0,4
111461	SOX4 Protein	SOX4	0,4
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,4
220451	Zinc Finger protein 144	ZNF144	0,5
125413	Mucin 1	MUC1	0,6
290007	CD44 antigen, epithelial form	CD44	0,6
108571	Retinoblastoma-Like 2 (p130)	RBL2	0,7
130788	Topoisomerase (DNA) II Beta (180kD)	TOP2B	0,7

### Gene clusters

Gene clustering from Fig. 2b showed groups of genes with correlated expression across samples. When different clones represented the same gene, they were

clustered next to each other (red arrows). Correlation coefficients between gene pairs in the 34 tumors were often high (1% of the 13,041 gene pairs showed a correlation coefficient superior to 0.95 - not shown). An example of highly correlated gene expression is that of BCL2 and RBL2. Such correlated expression, although it has not been described in the literature, probably reflects a common mechanism of regulation for these two genes. Furthermore, these genes also exhibited significant correlated expression with other genes such as PPP2CA, AKT2, PRKCSH or TNFRSF6/FAS. In particular, a striking correlated expression between BCL2 and FAS could be observed ( $r = 0.91$ ; data not shown). The exact meaning of this correlation is unknown, although it may reflect the necessary balance between apoptosis and anti-apoptosis for cell survival.

Although in human cancer the proportion of changes that is reflected at the RNA level is not known, monitoring gene expression patterns appears as a very promising way of increasing the knowledge of the disease. Several different types of cancer have been investigated using cDNA arrays: cervical (14), hepatocellular (15), ovarian (16), colon (17) and renal carcinomas (18), glioblastomas (19), melanomas (20) (21), rhabdomyosarcomas (22), acute leukemias (23) and lymphomas (24). In breast cancer, pioneering studies have yielded the first expression patterns (4, 25-31). They have in particular addressed the important issue of molecular differences in hormone responsive and non-responsive breast tumors. Thus, Yang et al. (28) and Hoch et al. (25) compared expression profiles of breast carcinoma cell lines known to represent these two categories and identified a few genes with differential expression. One of these genes was GATA3. In these studies, cell lines were mostly used and tumor samples were rarely

tested and generally in small numbers. The first study analyzing the expression profiles of a large series of breast cancers was published recently (32), but no correlation with clinical outcome was mentioned.

5               Several interesting points can be made based on the present experimentation. First, the differences in expression patterns among the tumors provided molecular transcriptional evidence of the histoclinical heterogeneity of breast cancer. This diversity was multifactorial, linked  
10 to many different genes, highlighting the interest of high throughput analysis in this context. It was possible, with a hierarchical clustering program integrating the expression profiles, to separate normal breast tissue from most tumors and, moreover, to identify two different groups of tumors.  
15 Most importantly, two different subgroups of tumors with a very distinct clinical outcome that could not be predicted with classical prognostic factors have been identified by clustering. Indeed, all these tumors had a theoretically bad prognosis as evaluated by current histoclinical tools. All  
20 these patients would be at the present time treated with adjuvant chemotherapy, but without the capacity for the physicians to identify patients who will benefit of this treatment and those who will not benefit.

Gene expression profiles were able to make this  
25 discrimination. Such predictive tools have important therapeutic implications. Patients with features of poor prognosis are candidates for other treatment than standard chemotherapy, avoiding loss of time and toxicities related to first-line chemotherapy. These results suggest that the  
30 histoclinical category of poor prognosis breast cancer, currently treated with adjuvant anthracyclin-based chemotherapy, groups together at least two molecularly distinct subgroups of tumors with different outcome which

would require distinct chemotherapy regimens. Expression profiles could thus provide a new and more accurate way of classifying breast tumors of poor prognosis and managing patients.

5                   Similarly, despite molecular heterogeneity, significant correlations between the expression level of genes (GATA3, ERBB2) and histological tumor parameters were identified. The ER-positivity in breast cancer has been correlated with tumor differentiation, low proliferating  
10 rate, favorable prognosis and response to hormonal therapy. The relation between hormone sensitivity of breast cancer and ER status is not perfect, and it is possible that some genes related to ER expression are more important than ER to characterize the hormone sensitive phenotype. These genes  
15 could serve as predictive factors to guide the therapy.

GATA3 mRNA expression was highly correlated with ER status. GATA3, which is not estrogen-regulated (25), is a transcription factor that could regulate the expression of genes involved in the ER-positive phenotype. Among the other  
20 genes that were found associated with ER status during the experimental work leading to the present invention, some, such as MYB (10), stromelysin 3 (33), and CRABP2 (34), have been previously reported expressed at high levels in ER-positive breast tumors. The higher levels of TP53 mRNA in  
25 ER-positive tumors studied were surprising, although in agreement with a recent study (27). Most studies concerning TP53 expression analyzed the protein level rather than the mRNA level, and TP53 protein levels are classically negatively correlated with the ER status (35). The high  
30 expression of CRABP2 could be related to the better differentiated status of the ER-positive tumors. The low expression of the three immunity-related genes IL2RB, IL2RG and CD3G may be related to the low lymphoid infiltration in

these well differentiated tumors. ERBB2 high expression in breast cancer has been associated with a poor prognosis and some resistance to hormonal therapy and chemotherapy (36). It is involved in the regulation of cellular differentiation, adhesion, and motility. The motility-enhancing activity of ERBB2 (37) could be responsible for the increased metastatic potential and the unfavorable prognosis of the breast tumors that overexpress ERBB2. The low expression of E-cadherin and thrombospondin 1 in node-positive tumors are consistent with their putative role in different steps of metastatic spread: E-cadherin is an epithelial cell adhesion molecule whose disturbance is a prerequisite for the release of invasive cells in carcinomas (38) and thrombospondin 1 inhibits angiogenesis (39). Similarly, the high expression of the molecule surface antigen Mucin 1 in node-positive tumors (40) can reduce cell-cell interactions facilitating cell detachment and metastasis. CD44, encoding a transmembrane glycoprotein involved in cell adhesion and lymph node homing (41) was expressed at high levels in node-positive tumors as well as GSTP1 (Glutathione-S-Transferase Pi), recently reported associated with increased tumor size (27).

Second, there were a number of genes with highly correlated expression patterns. Gene correlations have already been reported with larger series of genes, essentially under dynamic experimental conditions (42) and recently in steady states (17). Here, correlations were based on expression profiles of a relatively small but selected series of genes and in steady states represented by different breast tumors. Gene correlations are potentially useful tools for cancer research in two ways: i)- they can provide information about the general regulation circuitry of a cancerous cell, allowing the identification of regulatory elements controlling expression networks; ii)- they offer the



possibility of reducing the complexity of the system analyzed by replacing, for example, the intensities of a large number of genes present in a gene cluster by their respective mean intensities.

5                   Finally, these results highlight the great potential of cDNA array in cancer research. The gene expression profiles confirmed the heterogeneity of breast cancer, and most importantly allowed us to identify, among a  
10                   series of poor prognosis breast tumors, two subtypes of the disease not yet recognized with usual histoclinical parameters but with a different clinical outcome after adjuvant chemotherapy. Furthermore, the present invention allows detecting genes of which expression was correlated with classical prognostic factors.

15                   Table 4 displays a library of polynucleotides SEQ ID NO :1 to SEQ ID NO : 468 corresponding to a population of polynucleotide sequences underexpressed or overexpressed in cells derived from tumors, more particularly breast tumors,  
20                   and their respective complements.

TABLE 4

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
HRB	1	hiv-1 rev binding protein	SEQ ID No:1		SEQ ID No:2
GATA1	2	gata-binding protein 1 (globin transcription factor 1)		SEQ ID No:3	SEQ ID No:4
TLK2	3	tousled-like kinase 2		SEQ ID No:5	SEQ ID No:6
EST T81919	4	ests, weakly similar to alu7_human alu subfamily sq sequence contamination warning entry [h.sapiens]	SEQ ID No:7	SEQ ID No:8	
CCND1	5	cyclin d1 (prad1: parathyroid adenomatosis 1)	SEQ ID No:9		SEQ ID No:10
STAT1	6	signal transducer and activator of transcription 1, 91kd		SEQ ID No:11	SEQ ID No:12
FGFR2	7	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome)	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
EST T89980	8	ests	SEQ ID No:16		
PPP3CC	9	protein phosphatase 3 (formerly 2b), catalytic subunit, gamma isoform (calcineurin a gamma)	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
EST T90726	10	ests	SEQ ID No:20	SEQ ID No:21	
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
RNF5	12	ring finger protein 5		SEQ ID No:25	SEQ ID No:26
AXL	13	axl receptor tyrosine kinase	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
PPP4C	15	protein phosphatase 4 (formerly x), catalytic subunit	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EST T79867	16	ests	SEQ ID No:35		
FGFR4	17	fibroblast growth factor receptor 4	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(autotaxin)			
RELA	19	v-rel avian reticuloendotheliosis viral oncogene homolog a (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3 (p65))	SEQ ID No:42		SEQ ID No:43
ITK	20	il2-inducible t-cell kinase		SEQ ID No:44	SEQ ID No:45
TNXB	21	tenascin xb		SEQ ID No:46	SEQ ID No:47
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
APC	24	adenomatosis polyposis coli	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
SYK	29	spleen tyrosine kinase	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
IL7R	30	interleukin 7 receptor		SEQ ID No:71	SEQ ID No:72
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GRB7	33	growth factor receptor-bound protein 7	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
CASP4	35	caspase 4, apoptosis-related cysteine protease	SEQ ID No:84		SEQ ID No:85
TIMP2	36	tissue inhibitor of metalloproteinase 2		SEQ ID No:86	SEQ ID No:87
DDT	37	d-dopachrome tautomerase	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
PRL	38	prolactin	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:91	No:92	No:93
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
PGF	42	placental growth factor, vascular endothelial growth factor-related protein		SEQ ID No:102	SEQ ID No:103
UBE3A	43	ubiquitin protein ligase e3a (human papilloma virus e6-associated protein, angelman syndrome)		SEQ ID No:104	SEQ ID No:105
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
TIE	45	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains		SEQ ID No:109	SEQ ID No:110
AMFR	46	autocrine motility factor receptor	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
EST R81127	47	homo sapiens mrna; cdna dkfzp434c136 (from clone dkfzp434c136)	SEQ ID No:114		
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
MDM2	50	mouse double minute 2, human homolog of; p53-binding protein		SEQ ID No:120	SEQ ID No:121
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
HIP-55	52	src homology 3 domain-containing protein hip-55	SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
CTSD	53	cathepsin d (lysosomal aspartyl protease)	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
IGF1R	54	insulin-like growth factor 1 receptor		SEQ ID No:129	SEQ ID No:130
INSR	55	insulin receptor		SEQ ID No:131	SEQ ID No:132
FOXO1A	56	forkhead box o1a (rhabdomyosarcoma)		SEQ ID No:133	SEQ ID No:134
EGFR	57	epidermal growth factor receptor	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	No:135	No:136	No:137
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
TNFRSF6	59	tumor necrosis factor receptor superfamily, member 6	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CDKN1A	60	cyclin-dependent kinase inhibitor 1a (p21, cip1)	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
GAPD	62	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
JUNB	63	jun b proto-oncogene	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ACVRL1	65	activin a receptor type ii-like 1	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
RIL	66	lim domain protein		SEQ ID No:162	SEQ ID No:163
SHC1	67	shc (src homology 2 domain-containing) transforming protein 1		SEQ ID No:164	SEQ ID No:165
GAPD	68	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
CSNK2B	70	casein kinase 2, beta polypeptide		SEQ ID No:171	SEQ ID No:172
GLG1	71	golgi apparatus protein 1	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
EDNRB	72	endothelin receptor type b		SEQ ID No:176	SEQ ID No:177
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
FGFR1	74	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome)	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
PPP2CA	75	protein phosphatase 2 (formerly 2a), catalytic subunit, alpha isoform		SEQ ID No:183	SEQ ID No:184
EST R55460	76	homo sapiens, clone image:4054156, mRNA, partial cds		SEQ ID No:185	

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
MC1R	78	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)		SEQ ID No:187	SEQ ID No:188
NRG1	79	neuregulin 1	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
CNTFR	80	ciliary neurotrophic factor receptor		SEQ ID No:192	SEQ ID No:193
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
ENG	82	endoglin (osler-rendu-weber syndrome 1)	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
HRMT1L1	84	hmt1 (hmrnp methyltransferase, s. cerevisiae)-like 1	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
ETV4	85	ets variant gene 4 (ela enhancer-binding protein, elaf)	SEQ ID No:204	SEQ ID No:205	
ANXA11	86	annexin a11		SEQ ID No:206	SEQ ID No:207
PDGFRB	87	platelet-derived growth factor receptor, beta polypeptide		SEQ ID No:208	SEQ ID No:209
WBSCR14	88	williams-beuren syndrome chromosome region 14		SEQ ID No:210	SEQ ID No:211
CD74	89	cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated)		SEQ ID No:212	SEQ ID No:213
ANXA7	90	annexin a7		SEQ ID No:214	SEQ ID No:215
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PTPN2	92	protein tyrosine phosphatase, non-receptor type 2	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
EPHA2	93	epha2	SEQ ID No:221		SEQ ID No:222
TIMP1	94	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
GRB2	97	growth factor receptor-bound protein 2	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
JUND	98	jun d proto-oncogene	SEQ ID No:233		SEQ ID No:234
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
THBS3	101	thrombospondin 3	SEQ ID No:240		SEQ ID No:241
ACTG1	102	actin, gamma 1	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	103	integrin, alpha 6	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
RAD9	104	rad9 (s. pombe) homolog	SEQ ID No:248		SEQ ID No:249
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
AKT2	106	v-akt murine thymoma viral oncogene homolog 2	SEQ ID No:253		SEQ ID No:254
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
SELE	109	selectin e (endothelial adhesion molecule 1)	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
PRKCSH	111	protein kinase c substrate 80k-h		SEQ ID No:263	SEQ ID No:264
DTR	112	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)		SEQ ID No:265	SEQ ID No:266
ITGB2	113	integrin, beta 2 (antigen cd18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)		SEQ ID No:267	SEQ ID No:268
NEO1	114	neogenin (chicken) homolog 1		SEQ ID No:269	SEQ ID No:270
POU2F2	115	pou domain, class 2, transcription	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		factor 2	No:271		No:272
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
PTK2	121	ptk2 protein tyrosine kinase 2		SEQ ID No:284	SEQ ID No:285
CDK4	122	cyclin-dependent kinase 4	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
BTF3	123	basic transcription factor 3	SEQ ID No:289		SEQ ID No:290
CSF1R	124	colony stimulating factor 1 receptor, formerly mcdonough feline sarcoma viral (v-fms) oncogene homolog	SEQ ID No:291		SEQ ID No:292
FLI1	125	friend leukemia virus integration 1	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
ETV5	127	ets variant gene 5 (ets-related molecule)	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4	128	cyclin-dependent kinase 4	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
YES1	129	v-yes-1 yamaguchi sarcoma viral oncogene homolog 1	SEQ ID No:303		SEQ ID No:304
IFI75	130	interferon-induced protein 75, 52kd	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
TGFBR3	132	transforming growth factor, beta receptor iii (betaglycan, 300kd)	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
PRDX2	133	peroxiredoxin 2	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
FOS	134	v-fos fbj murine osteosarcoma viral oncogene homolog		SEQ ID No:317	SEQ ID No:318



Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RBBP7	135	retinoblastoma-binding protein 7	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
KIAA107 5	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
ABCC5	137	atp-binding cassette, sub-family c (cftr/mrp), member 5		SEQ ID No:324	SEQ ID No:325
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
PCNA	143	proliferating cell nuclear antigen	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MGC1307 1	146	hypothetical protein mgc13071	SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
ILF2	147	interleukin enhancer binding factor 2, 45kd		SEQ ID No:350	SEQ ID No:351
FLJ1130 7	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
ZNF9	150	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	SEQ ID No:356		SEQ ID No:357
CREM	151	camp responsive element modulator	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
ETV5	155	ets variant gene 5 (ets-related	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		molecule)	No:368	No:369	No:300
CD69	156	cd69 antigen (p60, early t-cell activation antigen)		SEQ ID No:370	SEQ ID No:371
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
MXI1	160	max-interacting protein 1		SEQ ID No:380	SEQ ID No:381
HOXA5	161	homeo box a5	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TNFAIP3	163	tumor necrosis factor, alpha-induced protein 3	SEQ ID No:388	SEQ ID No:389	SEQ ID No:390
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
FOS	170	v-fos fbj murine osteosarcoma viral oncogene homolog	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RELB	175	v-rel avian reticuloendotheliosis viral oncogene homolog b (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3)	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1)	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	
ESTs H42957 & H42888	187	Human interleukin 3 receptor (hIL-3Ra)	SEQ ID No:440	SEQ ID No:441	
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442	SEQ ID No:443	
ERBB2	189	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	SEQ ID No:444		
ZNF144	190	zinc finger protein 144 (Mel-18) (ZNF144)	SEQ ID No:445		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
MARK3	191	MAP/microtubule affinity-regulating kinase 3 (MARK3)	SEQ ID No:446	SEQ ID No:447	
EST N68536	192	EST N68536 MAX-interacting protein 1 (MXI1)	SEQ ID No:448		
EST R81126	193	EST R81126 lymphotoxin beta receptor (LTBR)		SEQ ID No:449	
POU2F2	194	(POU2F2)		SEQ ID No:450	
CASP1	195	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)		SEQ ID No:451	
HRB	196	syndecan 1 (SDC1) (ex HRB)		SEQ ID No:452	
ITGB2	197	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	SEQ ID No:453		
MGST1	198	protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)		SEQ ID No:454	
PPP2CA	199	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	SEQ ID No:455		
SUI1	200	S100 calcium-binding protein A11 (calgizzarin) (S100A11)		SEQ ID No:456	
GZMA	201	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA)		SEQ ID No:457	
EDN1	202	endothelin 1 (EDN1)	SEQ ID No:458		
PTPN6	203	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	SEQ ID No:459		
TFAP4	204	transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)	SEQ ID No:460		
CCND2	205	cyclin D2 (CCND2)	SEQ ID No:461		
JUP	206	junction plakoglobin (JUP)	SEQ ID No:462		
GADD45A	207	growth arrest and DNA-damage-inducible, alpha (GADD45A)	SEQ ID No:463		
nm23	208	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	SEQ ID No:464		
BBC1	209	ribosomal protein L13 (RPL13) (ex	SEQ ID		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		BBC1)	No:465		
VEGFB	210	vascular endothelial growth factor B (VEGFB)	SEQ ID No:466		
LAMR1	211	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	SEQ ID No:467		
CSH1	212	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor		SEQ ID No:468	

Tables 5A and 5B hereunder displays two subpopulations corresponding to the 5 top overexpressed and to the 5 top underexpressed polynucleotide sequences particularly interesting to distinguish healthy person from cancer patient.

TABLE 5A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		

TABLE 5B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
PRL	38	prolactin	SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		

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Table 6 hereunder relate to sub populations of polynucleotide sequences interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER-samples.

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TABLE 6

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBPI	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442		

Tables 6A et 6B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples

**Table 6A**  
overexpressed genes : top 5  
ER + / ER -

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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**Table 6B**  
underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 7 hereunder relates to subpopulations of polynucleotide sequences interesting to distinguish tumors with lymph node from tumors with no lymph node.



TABLE 7

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T89980	8	ests	SEQ ID No:16		
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	

Tables 7A and 7B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors with lymph node from tumors with no lymph node.

**TABLE 7A**

Overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252

**TABLE 7B**

Underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336

Tables 8, 8A and 8B hereunder relates to sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

**TABLE 8**

A1 /A2

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	

Tables 8A and 8B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

**TABLEAU 8A**

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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**TABLEAU 8B**

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 9, 9A and 9B hereunder relates to sub populations of polynucleotide sequences particularly interesting in classifying good and poor prognosis primary breast tumors.

TABLE 9

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:275		No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
BS69	144	adenovirus 5 e1a binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		cephalopolysyndactyly syndrome)			
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9A

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117



Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDI A	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9B

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
EST W73386	168	ests	SEQ ID No:401		

Overexpression of genes detected by using at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A combined with underexpression of genes detected with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B present a Good outcome.

So, a preferred DNA array according to the invention comprises at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A and at least

one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B.

5       Such DNA arrays are particularly useful to distinguish patients having a high risk (Bad Outcome) from those having a good pronostic (Good Outcome).

TABLE 10

CORRELATION BETWEEN SEQ ID NO AS FILED WITH US PROVISIONAL APPLICATION N° 60/254,090  
and SEQ ID NO FILED WITH PCT APPLICATION

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
GATA3	1	GATA-binding protein 3 (GATA3)	129757	SEQ ID No : 1		SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
MYB	2	v-myb avian myeloblastosis viral oncogene homolog (MYB)	248613		SEQ ID No : 2	0	SEQ ID No:354	SEQ ID No:355
KIAA1075	3	KIAA1075 protein	211999	SEQ ID No : 3	SEQ ID No : 4	SEQ ID No:322	SEQ ID No:323	0
STMV3	4	matrix metalloproteinase 11 (stromelysin 3) (MMP11) (ex STMV3)	235947	SEQ ID No : 5		SEQ ID No:345	0	SEQ ID No:346
HGFL	5	macrophage-stimulating protein (MST1) (ex HGFL)	229839	SEQ ID No : 6	SEQ ID No : 7	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
CRABP	6	cellular retinoic acid-binding protein 2 (CRABP2)	153275	SEQ ID No : 8	SEQ ID No : 9	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
XBP1	7	X-box binding protein 1 (XBP1)	301950	SEQ ID No : 10	SEQ ID No : 11	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TP53	8	tumor protein p53 (LI-Fraumeni syndrome) (TP53)	205314		SEQ ID No : 12	SEQ ID No:442	0	0
IGF2	9	insulin-like growth factor 2 (somatomedin A) (IGF2)	126233	SEQ ID No : 13	SEQ ID No : 14	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
CD3G	10	CD3G antigen, gamma polypeptide (T1T3 complex) (CD3G)	66322	SEQ ID No : 15	SEQ ID No : 16	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
IL2RG	11	interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG)	195022	SEQ ID No : 17	SEQ ID No : 18	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
SOX4	12	SRY (sex determining region Y)-box 4 (SOX4)	111461	SEQ ID No : 19	SEQ ID No : 20	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
EGFR	13	epidermal growth factor receptor (avian erythroblastic)	151475	SEQ ID No : 21	SEQ ID No : 22	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
TOP2B	14	topoIIb mRNA for topoisomerase IIb.	130788		SEQ ID No : 23	0	SEQ ID No:82	SEQ ID No:83
S100B	15	S100 calcium-binding protein, beta (neural) (S100B)	183641		SEQ ID No : 24	0	SEQ ID No:255	SEQ ID No:256
EST N53133	16	EST N53133	246620	SEQ ID No : 25		SEQ ID No:352	0	SEQ ID No:353
GSTP1	17	glutathione S-transferase pI (GSTP1)	231424	SEQ ID No : 26	SEQ ID No : 27	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
THBS1	18	thrombospondin 1 (THBS1)	160963	SEQ ID No : 28		SEQ ID No:216	0	SEQ ID No:217

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
PDPN2	19	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autolysin) (ENPP2) (ex PDPN2)	120916	SEQ ID No : 29	SEQ ID No : 30	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
ATF3	20	activating transcription factor 3 (ATF3)	183030	SEQ ID No : 31	SEQ ID No : 32	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
NF1A	21	(ex NF1A)	110480	SEQ ID No : 33		SEQ ID No:16	0	0
SELP	22	selectin P (granule membrane protein 140kD, antigen CD62) (SELP)	182264		SEQ ID No : 34	SEQ ID No:438	SEQ ID No:439	0
CDH1	23	cadherin 1, E-cadherin (epithelial) (CDH1)	214008	SEQ ID No : 35	SEQ ID No : 36	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ERBB2	24	y-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	147016	SEQ ID No : 37		0	SEQ ID No:118	SEQ ID No:119
PP2A BR gamma	25	(PP2A BR gamma)	179197	SEQ ID No : 38	SEQ ID No : 39	SEQ ID No:238	SEQ ID No:239	0
ZNF144	26	zinc finger protein 144 (Mel-18) (ZNF144)	220451	SEQ ID No : 40	SEQ ID No : 41	0	SEQ ID No:329	SEQ ID No:330
MUC1	27	mucin 1, transmembrane (MUC1)	125413		SEQ ID No : 42	0	SEQ ID No:57	SEQ ID No:58
CD44	28	CD44E (epithelial form)	290007	SEQ ID No : 43	SEQ ID No : 44	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
PLA2G2A	29	phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A), nuclear gene encoding mitochondrial protein	152802	SEQ ID No : 45	SEQ ID No : 46	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
ACVRL1	30	activin A receptor type II-like 1 (ACVRL1)	153350	SEQ ID No : 47	SEQ ID No : 48	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
AXL	31	AXL receptor tyrosine kinase (AXL)	112500	SEQ ID No : 49	SEQ ID No : 50	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
PKU-ALPHA	32	KU-alpha, partial cds (new gene symbol Tik2)	109569		SEQ ID No : 51	0	SEQ ID No:5	SEQ ID No:6
ABCC5	33	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)	212366		SEQ ID No : 52	0	SEQ ID No:324	SEQ ID No:325
EDNRB	34	endothelin receptor type B (EDNRB), transcript variant1	154244		SEQ ID No : 53	0	SEQ ID No:176	SEQ ID No:177
DTR	35	diphtheria toxin receptor (heparin-binding epidermal)	187547		SEQ ID No : 54	0	SEQ ID No:265	SEQ ID No:266
IGF1R	36	insulin-like growth factor 1 receptor (IGF1R)	150361		SEQ ID No : 55	0	SEQ ID No:129	SEQ ID No:130
KIAA0427	37	KIAA0427	127507	SEQ ID No : 56	SEQ ID No : 57	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
CD69	38	CD69 antigen (p60, early T-cell activation antigen)	276727		SEQ ID No : 58	0	SEQ ID No:370	SEQ ID No:371
FGFR4	39	fibroblast growth factor receptor 4 (FGFR4)	116781	SEQ ID No : 59	SEQ ID No : 60	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
EST T85683	40	EST T85683 cathepsin B (CTSB)	112822		SEQ ID No : 61	0	SEQ ID No:30	SEQ ID No:31
EST R00569	41	EST R00569 IL2-inducible T-cell kinase (ITK)	123871		SEQ ID No : 62	0	SEQ ID No:44	SEQ ID No:45

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TGFB3	42	transforming growth factor, beta receptor III (TGFB3)	208118	SEQ ID No : 63	SEQ ID No : 64	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
INSR	43	insulin receptor (INSR)	151149		SEQ ID No : 65	0	SEQ ID No:131	SEQ ID No:132
MARK3	44	MAP/microtubule affinity-regulating kinase 3 (MARK3)	110599	SEQ ID No : 66	SEQ ID No : 67	#N/A	#N/A	#N/A
TIMP2	45	tissue inhibitor of metalloproteinase 2 (TIMP2)	131504		SEQ ID No : 68	0	SEQ ID No:86	SEQ ID No:87
EST R85557	46	EST R85557 thrombospondin 3 (THBS3)	180219	SEQ ID No : 69		SEQ ID No:240	0	SEQ ID No:241
GNRH1	47	gonadotropin-releasing hormone 1 (GNRH1)	192688		SEQ ID No : 70	0	SEQ ID No:277	SEQ ID No:278
FGFR2	48	fibroblast growth factor receptor 2 (FGFR2)	110387	SEQ ID No : 71	SEQ ID No : 72	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
NFKB2	49	NFKB2	114879	SEQ ID No : 73		SEQ ID No:35	0	0
VIL2	50	villin 2 (ezrin) (VIL2)	124701	SEQ ID No : 74	SEQ ID No : 75	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
ENG	51	endoglin (ENG)	156979	SEQ ID No : 76	SEQ ID No : 77	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EPHA2	52	Epha2 (EPHA2)	162004	SEQ ID No : 78		SEQ ID No:221	0	SEQ ID No:222
CREM	53	cAMP responsive element modulator (CREM)	258584	SEQ ID No : 79	SEQ ID No : 80	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
ETV5-a	54	ets variant gene 5 (ETV5)	270549	SEQ ID No : 81	SEQ ID No : 82	SEQ ID No:368	SEQ ID No:369	SEQ ID No:300
EST N68536	55	EST N68536 MAX-interacting protein 1 (MXI1)	298242	SEQ ID No : 83	SEQ ID No : 84	0	SEQ ID No:380	SEQ ID No:381
EST R81126	56	EST R81126 lymphotoxin beta receptor (LTBR)	146635	SEQ ID No : 85	SEQ ID No : 86	SEQ ID No:114	0	0
POU2F2	57	POU2F2	188393	SEQ ID No : 87	SEQ ID No : 88	SEQ ID No:271	0	SEQ ID No:272
FLI1	58	Friend leukemia virus integration 1 (FLI1)	198144	SEQ ID No : 89	SEQ ID No : 90	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
TIE	59	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE)	144081		SEQ ID No : 91	0	SEQ ID No:109	SEQ ID No:110
PRLR	60	prolactin receptor (PRLR)	138788	SEQ ID No : 92	SEQ ID No : 93	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
PPP3CA	61	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC) (ex PPP3CA)	110481	SEQ ID No : 94	SEQ ID No : 95	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
PTPN2	62	protein tyrosine phosphatase, non-receptor type 2 (PTPN2)	161451	SEQ ID No : 96	SEQ ID No : 97	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
PGF	63	placental growth factor, vascular endothelial growth factor-related protein (PGF)	139326		SEQ ID No : 98	0	SEQ ID No:102	SEQ ID No:103
TNFAIP3	64	tumor necrosis factor, alpha-induced	309943	SEQ ID No : 99		SEQ ID No:388	SEQ ID No:389	SEQ ID No:390

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		protein 3 (TNFAIP3)						
PHB	65	PHB (prohibitin)	236008	SEQ ID No : 100		SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
RIL	66	LIM domain protein (RIL)	153446		SEQ ID No : 101	0	SEQ ID No:162	SEQ ID No:163
MYBL2	67	v-myb avian myeloblastosis viral oncogene homolog-like 2 (MYBL2)	207378	SEQ ID No : 102	SEQ ID No : 103	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
RELB	68	v-rel avian reticuloendotheliosis oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3) (RELB)	66969	SEQ ID No : 104	SEQ ID No : 105	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
EST R97218	69	Est R97218	200394	SEQ ID No : 106		SEQ ID No:296	SEQ ID No:297	0
GZMH	70	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB) (ex GZMH)	154343	SEQ ID No : 107		SEQ ID No:178	0	SEQ ID No:179
MYC	71	c-myc proto-oncogene	129438	SEQ ID No : 108	SEQ ID No : 109	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
CASP1	72	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)	131502		SEQ ID No : 110	SEQ ID No:84	0	SEQ ID No:85
SYK	73	spleen tyrosine kinase (SYK)	128142	SEQ ID No : 111	SEQ ID No : 112	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
EST H27202	74	EST H27202 transcription factor E1AF gene	158347	SEQ ID No : 113	SEQ ID No : 114	SEQ ID No:204	SEQ ID No:205	0
HRB	75	syndecan 1 (SDC1) (ex HRB)	108490	SEQ ID No : 115	SEQ ID No : 116	SEQ ID No:1	0	SEQ ID No:2
SHC1	76	p86shc (SHC)	153548		SEQ ID No : 117	0	SEQ ID No:164	SEQ ID No:165
CSF1	77	colony stimulating factor 1 (CSF1)	124554	SEQ ID No : 118	SEQ ID No : 119	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
UBE3A	78	ubiquitin protein ligase E3A (UBE3A)	141924		SEQ ID No : 120	0	SEQ ID No:104	SEQ ID No:105
FKHR	79	forkhead box O1A (rhabdomyosarcoma) (FOXO1A) (ex FKHR)	151247		SEQ ID No : 121	0	SEQ ID No:133	SEQ ID No:134
CSF1R	80	colony stimulating factor 1 receptor (CSF1R)	196282	SEQ ID No : 122		SEQ ID No:291	0	SEQ ID No:292
IFI75	81	interferon-induced protein 75 (IFI75)	205612	SEQ ID No : 123	SEQ ID No : 124	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
GATA1	82	GATA-binding protein 1 (globin transcription factor 1) (GATA1)	109093		SEQ ID No : 125	0	SEQ ID No:3	SEQ ID No:4
STAT1	83	signal transducer and activator of transcription 1 (STAT1)	110101		SEQ ID No : 126	0	SEQ ID No:11	SEQ ID No:12
CREBBP	84	CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP)	109677	SEQ ID No : 127	SEQ ID No : 128	SEQ ID No:7	SEQ ID No:8	0
IL7R	85	interleukin 7 receptor (IL7R)	129059		SEQ ID No : 129	0	SEQ ID No:71	SEQ ID No:72
ANXA7	86	annexin A7 (ANXA7)	160580		SEQ ID No : 130	0	SEQ ID No:214	SEQ ID No:215

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TNXA	87	tenascin XA (TNXA)	124340		SEQ ID No : 131	0	SEQ ID No:46	SEQ ID No:47
CNBP1	88	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9) (ex CNBP1)	251963	SEQ ID No : 132		SEQ ID No:356	0	SEQ ID No:357
CDK4-a	89	cyclin-dependent kinase 4 (CDK4)	204586	SEQ ID No : 133	SEQ ID No : 134	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
CSNK2B	90	gene for casein kinase II subunit beta (EC 2.7.1.37)	153879		SEQ ID No : 135	0	SEQ ID No:171	SEQ ID No:172
EFNA1	91	ephrin-A1 (EFNA1)	162997		SEQ ID No : 136	0	SEQ ID No:226	SEQ ID No:227
SELE	92	selectin E (endothelial adhesion molecule 1) (SELE)	186132	SEQ ID No : 137	SEQ ID No : 138	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
APC	93	adenomatosis polyposis coli (APC)	125294	SEQ ID No : 139	SEQ ID No : 140	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
FAK	94	PTK2 protein tyrosine kinase 2 (PTK2) (ex FAK)	195731		SEQ ID No : 141	0	SEQ ID No:284	SEQ ID No:285
FOS-a	95	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	208717		SEQ ID No : 142	0	SEQ ID No:317	SEQ ID No:318
FGFR1	96	fibroblast growth factor receptor (FGFR)	154472	SEQ ID No : 143	SEQ ID No : 144	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
MC1R	97	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor) (MC1R)	155691		SEQ ID No : 145	0	SEQ ID No:187	SEQ ID No:188
PCNA	98	proliferating cell nuclear antigen (PCNA)	232941	SEQ ID No : 146	SEQ ID No : 147	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
DDT	99	D-dopachrome tautomerase (DDT)	132109	SEQ ID No : 148	SEQ ID No : 149	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
GRB2	100	growth factor receptor-bound protein 2 (GRB2)	172152	SEQ ID No : 150	SEQ ID No : 151	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
AMFR	101	autocrine motility factor receptor (AMFR)	146280	SEQ ID No : 152	SEQ ID No : 153	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
ITGB2	102	integrin, beta 2 (antigen CD18 (p85), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	187822	SEQ ID No : 154		0	SEQ ID No:267	SEQ ID No:268
JUND	103	jun D proto-oncogene (JUND)	175421	SEQ ID No : 155		SEQ ID No:233	0	SEQ ID No:234
NF45	104	interleukin enhancer binding factor 2 (ILF2) (ex NF45)	243907		SEQ ID No : 156	0	SEQ ID No:350	SEQ ID No:351
PPP4C	105	protein phosphatase 4 (formerly X) (PPP4C)	114097	SEQ ID No : 157	SEQ ID No : 158	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EMS1	106	ATX1 (antioxidant protein 1, yeast homolog 1 (ATOX1) (ex EMS1))	149172	SEQ ID No : 159		SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
BCL2	107	B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha	147002	SEQ ID No : 160	SEQ ID No : 161	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
MGST1	108	protein phosphatase 1, catalytic subunit,	162610	SEQ ID No : 162	SEQ ID No : 163	SEQ ID No:248	0	SEQ ID No:249



Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		alpha isoform (PPP1CA) (ex MGST1)						
PDGFRB	109	platelet-derived growth factor receptor, beta polypeptide (PDGFRB)	158976		SEQ ID No : 164	0	SEQ ID No:208	SEQ ID No:209
ANXA11	110	annexin A11 (ANXA11)	158892		SEQ ID No : 165	0	SEQ ID No:206	SEQ ID No:207
GPX1	111	histocompatibility class II antigen gamma chain (CD74) (ex GPX1 Glutathion S transférase)	159809		SEQ ID No : 166	0	SEQ ID No:212	SEQ ID No:213
CFR-1	112	Golgi apparatus protein 1 (GLG1) (ex CFR-1)	153974	SEQ ID No : 167	SEQ ID No : 168	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
BTF3L3	113	basic transcription factor 3 (BTF3)	195889	SEQ ID No : 169		SEQ ID No:289	0	SEQ ID No:290
EST R55460	114	EST R55460	154997		SEQ ID No : 170	0	SEQ ID No:185	0
AKT2	115	v-akt murine thymoma viral oncogene homolog 2 (AKT2)	183552	SEQ ID No : 171		SEQ ID No:253	0	SEQ ID No:254
CDKN1A	116	cyclin-dependent kinase inhibitor (CDKN1A)	152524	SEQ ID No : 172	SEQ ID No : 173	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PPP2CA	117	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	154685	SEQ ID No : 174	SEQ ID No : 175	0	SEQ ID No:183	SEQ ID No:184
MDM2	118	mouse double minute 2, human homolog of p53-binding protein (MDM2), transcript variant MDM2	148052	SEQ ID No : 176		0	SEQ ID No:120	SEQ ID No:121
TNFRSF6	119	tumor necrosis factor receptor superfamily, member 6 (TNFRSF6)	151767	SEQ ID No : 177	SEQ ID No : 178	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CNTFR	120	ciliary neurotrophic factor receptor (CNTFR)	156431		SEQ ID No : 179	0	SEQ ID No:192	SEQ ID No:193
JUNB	121	jun B proto-oncogene (JUNB)	153213	SEQ ID No : 180	SEQ ID No : 181	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CCND1	122	cyclin D1 (PRAD1; parathyroid adenomatosis 1) (CCND1)	110022	SEQ ID No : 182		SEQ ID No:9	0	SEQ ID No:10
TDPX1	123	peroxiredoxin 2 (PRDX2) (ex TDPX1)	208439	SEQ ID No : 183	SEQ ID No : 184	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
GRB7	124	growth factor receptor-bound protein 7 (GRB7)	130923	SEQ ID No : 185	SEQ ID No : 186	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
RBBP7	125	retinoblastoma-binding protein 7 (RBBP7)	210874	SEQ ID No : 187	SEQ ID No : 188	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
TIMP1	126	issue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1)	162246	SEQ ID No : 189	SEQ ID No : 190	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
YES1	127	y-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1)	204634	SEQ ID No : 191		SEQ ID No:303	0	SEQ ID No:304
RNF5	128	ring finger protein 5 (RNF5)	112098		SEQ ID No : 192	0	SEQ ID No:25	SEQ ID No:26
PRKCSH	129	protein kinase C substrate 80K-H (PRKCSH)	187232		SEQ ID No : 193	0	SEQ ID No:263	SEQ ID No:264

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
CTSD	130	cathepsin D (lysosomal aspartyl protease) (CTSD)	149401	SEQ ID No : 194	SEQ ID No : 195	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
NEO1	131	neogenin (chicken) homolog 1 (NEO1)	188380		SEQ ID No : 196	0	SEQ ID No:269	SEQ ID No:270
GAPD-a	132	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	152847			SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
ACTG1	133	actin, gamma 1 (ACTG1)	182291	SEQ ID No : 197		SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	134	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 198	SEQ ID No : 199	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
GAPD-b	135	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	153607	SEQ ID No : 200	SEQ ID No : 201	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
ETV5-b	136	ets variant gene 5 (ets-related molecule) (ETV5)	203394	SEQ ID No : 202	SEQ ID No : 203	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4-b	137	cyclin-dependent kinase 4 (CDK4)	195800	SEQ ID No : 204	SEQ ID No : 205	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
FOS-b	138	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	363796	SEQ ID No : 206	SEQ ID No : 207	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
HOXA5	139	homeobox protein (HOX-1.3) (ex Hox A5)	300564	SEQ ID No : 208	SEQ ID No : 209	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
RELA	140	NF-kappa-B transcription factor p65 DNA binding subunit (ex RELa)	122056	SEQ ID No : 210	SEQ ID No : 211	SEQ ID No:42	0	SEQ ID No:43
SUI1	141	S100 calcium-binding protein A11 (calgizzarin) (S100A11)	155345	SEQ ID No : 212	SEQ ID No : 213	SEQ ID No:186	0	0
ANG	142	angiotensin, ribonuclease, RNase A family, 5 (ANG)	156720		SEQ ID No : 214	0	SEQ ID No:194	SEQ ID No:195
ITGA6	143	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 215	SEQ ID No : 216	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
PRMT2	144	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 1 (HRMT1L1) (ex PRMT2)	158038	SEQ ID No : 217	SEQ ID No : 218	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
EST R55480	145	EST R55480	154997		SEQ ID No : 219	0	SEQ ID No:185	0
GZMA	146	granzyme A (granzyme 1, cytotoxic T- lymphocyte-associated serine esterase 3) (GZMA)	356763	SEQ ID No : 220	SEQ ID No : 221	SEQ ID No:402	0	SEQ ID No:403
SOX9	147	SRY (sex-determining region Y)-box 9 (campomelic dysplasia, autosomal sex- reversal) (SOX9)	323948	SEQ ID No : 222		SEQ ID No:394	0	SEQ ID No:395
SRF	148	serum response factor (c-fos serum response element-binding transcription factor) (SRF)	321329	SEQ ID No : 223	SEQ ID No : 224	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
EDN1	149	endothelin 1 (EDN1)	153424	SEQ ID No : 225		#N/A	#N/A	#N/A
PTPN6	150	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	66778	SEQ ID No : 226		#N/A	#N/A	#N/A
TFAP4	151	transcription factor AP-4 (activating)	159093	SEQ ID No : 227		0	SEQ ID No:210	SEQ ID No:211

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		enhancer binding protein 4) (TFAP4)						
ELF1	152	Human cis-acting sequence.Elf-1	182007	SEQ ID No : 228		SEQ ID No:437	0	0
CD2	153	CD2 antigen (p50), sheep red blood cell receptor (CD2)	120649	SEQ ID No : 229		SEQ ID No:431	0	0
CCND2	154	cyclin D2 (CCND2)	175256	SEQ ID No : 230		#N/A	#N/A	#N/A
IL3RA	155	interleukin 3 receptor (hIL-3Ra)	183087	SEQ ID No : 231		SEQ ID No:440	SEQ ID No:441	0
JUP	156	junction plakoglobin (JUP)	157958	SEQ ID No : 232		#N/A	#N/A	#N/A
RBL2	157	retinoblastoma-like 2 (p130) (RBL2)	108571	SEQ ID No : 233		SEQ ID No:430	0	0
HOXA4	158	homeo box A4 (HOXA4)	110731	SEQ ID No : 234		SEQ ID No:20	SEQ ID No:21	0
ACY1	159	aminoacylase 1 (ACY1)	160764	SEQ ID No : 235		SEQ ID No:435	SEQ ID No:436	0
GADD45A	160	growth arrest and DNA-damage-inducible, alpha (GADD45A)	115176	SEQ ID No : 236		#N/A	#N/A	#N/A
nm23	161	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	174388	SEQ ID No : 237		#N/A	#N/A	#N/A
BBC1	162	ribosomal protein L13 (RPL13) (ex BBC1)	178317	SEQ ID No : 238		#N/A	#N/A	#N/A
VEGFB	163	vascular endothelial growth factor B (VEGFB)	162499	SEQ ID No : 239		#N/A	#N/A	#N/A
LAMR1	164	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	199837	SEQ ID No : 240		#N/A	#N/A	#N/A
IL2RB	165	interleukin 2 receptor, beta (IL2RB)	139073	SEQ ID No : 241	SEQ ID No : 242	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
DES	166	desmin	153854	SEQ ID No : 243		SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
PRL	167	prolactin	133738	SEQ ID No : 244		SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
CSH1	168	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor	133891		SEQ ID No : 245	SEQ ID No:432	0	0
TEK	169	tyrosine protein kinase receptor	151501	SEQ ID No : 246	SEQ ID No : 247	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
Nrg1	170	neuregulin 1 (EST R72075)	155716	SEQ ID No : 248	SEQ ID No : 249	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
PLAT	rien	pas d'EST ni mRNA	160149			SEQ ID No:433	SEQ ID No:434	0
EST	rien		Image ?					
AW184517								

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## CLAIMS

1. A polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 or the complement thereof.

2. A polynucleotide library according to Claim 1 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in anyone of the following predefined sets :

SET 1: (SEQ ID No:1; SEQ ID No:2); SET 2: (SEQ ID No:3; SEQ ID No:4); SET 3: (SEQ ID No:5; SEQ ID No:6); SET 4: (SEQ ID No:7; SEQ ID No:8); SET 5: (SEQ ID No:9; SEQ ID No:10); SET 6: (SEQ ID No:11; SEQ ID No:12); SET 7: (SEQ ID No:13; SEQ ID No:14; SEQ ID No:15); SET 8: (SEQ ID No:16); SET 9: (SEQ ID No:17; SEQ ID No:18; SEQ ID No:19); SET 10: (SEQ ID No:20; SEQ ID No:21); SET 11: (SEQ ID No:22; SEQ ID No:23; SEQ ID No:24); SET 12: (SEQ ID No:25; SEQ ID No:26); SET 13: (SEQ ID No:27; SEQ ID No:28; SEQ ID No:29); SET 14: (SEQ ID No:30; SEQ ID No:31); SET 15: (SEQ ID No:32; SEQ ID No:33; SEQ ID No:34) ; SET 16 : (SEQ ID No:35) ; SET 17 : (SEQ ID No:36; SEQ ID No:37; SEQ ID No:38) ; SET 18 : (SEQ ID No:39; SEQ ID No:40; SEQ ID No:41) ; SET 19 : (SEQ ID No:42; SEQ ID No:43) ; SET 20 : (SEQ ID No:44; SEQ ID No:45) ; SET 21 : (SEQ ID No:46; SEQ ID No:47) ; SET 22 : (SEQ ID No:48; SEQ ID No:49; SEQ ID No:50) ; SET 23 : (SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET 24: (SEQ ID No:54; SEQ ID No:55; SEQ ID No:56) ; SET 25: (SEQ ID No:57; SEQ ID No:58) ; SET 26: (SEQ ID No:59; SEQ ID No:60; SEQ ID No:61) ; SET 27: (SEQ ID No:62; SEQ ID No:63; SEQ ID No:64) ; SET 28: (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;

SET 29: (SEQ ID No:68; SEQ ID No:69; SEQ ID No:70) ; SET 30: (SEQ ID No:71; SEQ ID No:72) ; SET 31 : (SEQ ID No:73; SEQ ID No:74; SEQ ID No:75) ; SET 32 : (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET 33 : (SEQ ID No:79; SEQ ID No:80; SEQ ID No:81) ; SET 34: (SEQ ID No:82; SEQ ID No:83) ; SET 35: (SEQ ID No:84; SEQ ID No:85) ; SET 36: (SEQ ID No:86; SEQ ID No:87) ; SET 37: (SEQ ID No:88; SEQ ID No:89; SEQ ID No:90) ; SET 38: (SEQ ID No:91; SEQ ID No:92; SEQ ID No:93) ; SET 39: (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET 40: (SEQ ID No:97; SEQ ID No:98; SEQ ID No:99) ; SET 41: (SEQ ID No:100; SEQ ID No:101; SEQ ID No:102) ; SET 42: (SEQ ID No:103; SEQ ID No:104; SEQ ID No:105) ; SET 43: (SEQ ID No:106; SEQ ID No:107; SEQ ID No:108) ; SET 44: (SEQ ID No:109; SEQ ID No:110) ; SET 45: (SEQ ID No:111; SEQ ID No:112; SEQ ID No:113) ; SET 46: (SEQ ID No:114; SEQ ID No:115; SEQ ID No:116; SEQ ID No:117) ; SET 47: (SEQ ID No:118; SEQ ID No:119) ; SET 48: (SEQ ID No:120; SEQ ID No:121) ; SET 49: (SEQ ID No:122; SEQ ID No:123; SEQ ID No:124; SEQ ID No:125) ; SET 50: (SEQ ID No:126; SEQ ID No:127; SEQ ID No:128) ; SET 51: (SEQ ID No:129; SEQ ID No:130) ; SET 52: (SEQ ID No:131; SEQ ID No:132) ; SET 53: (SEQ ID No:133; SEQ ID No:134) ; SET 54: (SEQ ID No:135; SEQ ID No:136; SEQ ID No:137) ; SET 55: (SEQ ID No:138; SEQ ID No:139; SEQ ID No:140) ; SET 56: (SEQ ID No:141; SEQ ID No:142; SEQ ID No:143) ; SET 57: (SEQ ID No:144; SEQ ID No:145; SEQ ID No:146) ; SET 58: (SEQ ID No:147; SEQ ID No:148; SEQ ID No:149) ; SET 59: (SEQ ID No:150; SEQ ID No:151; SEQ ID No:152) ; SET 60: (SEQ ID No:153; SEQ ID No:154; SEQ ID No:155) ; SET 61: (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET 62: (SEQ ID No:159; SEQ ID No:160; SEQ ID No:161) ; SET 63: (SEQ ID No:162; SEQ ID No:163) ; SET 64: (SEQ ID No:164; SEQ ID No:165) ; SET 65: (SEQ ID No:166; SEQ ID No:167; SEQ ID No:168) ; SET 66: (SEQ ID No:169; SEQ ID No:170) ; SET 67: (SEQ ID No:171; SEQ ID No:172) ; SET 68: (SEQ ID No:173; SEQ ID No:174; SEQ ID No:175) ; SET 69: (SEQ ID No:176; SEQ ID No:177) ; SET 70: (SEQ ID No:178; SEQ ID No:179) ; SET 71: (SEQ ID No:180; SEQ ID No:181; SEQ ID No:182) ; SET 72: (SEQ ID No:183; SEQ ID No:184) ; SET 73: (SEQ ID No:185) ; SET 74: (SEQ ID No:186) ; SET 75: (SEQ ID No:187; SEQ ID No:188) ; SET 76: (SEQ ID No:189)

SEQ ID No:190; SEQ ID No:191) ; SET 80: (SEQ ID No:192; SEQ ID  
No:193) ; SET 81: (SEQ ID No:194; SEQ ID No:195) ; SET 82: (SEQ ID  
No:196; SEQ ID No:197; SEQ ID No:198) ; SET 83: (SEQ ID No:199;  
SEQ ID No:200) ; SET 84: (SEQ ID No:201; SEQ ID No:202; SEQ ID  
5 No:203) ; SET 85: (SEQ ID No:204; SEQ ID No:205) ; SET 86: (SEQ ID  
No:206; SEQ ID No:207) ; SET 87: (SEQ ID No:208; SEQ ID No:209) ;  
SET 88: (SEQ ID No:210; SEQ ID No:211) ; SET 89: (SEQ ID No:212;  
SEQ ID No:213) ; SET 90: (SEQ ID No:214; SEQ ID No:215) ; SET 91:  
(SEQ ID No:216; SEQ ID No:217) ; SET 92: (SEQ ID No:218; SEQ ID  
10 No:219; SEQ ID No:220) ; SET 93: (SEQ ID No:221; SEQ ID No:222) ;  
SET 94: (SEQ ID No:223; SEQ ID No:224; SEQ ID No:225) ; SET 95:  
(SEQ ID No:226; SEQ ID No:227) ; SET 96: (SEQ ID No:228; SEQ ID  
No:229) ; SET 97: (SEQ ID No:230; SEQ ID No:231; SEQ ID No:232) ;  
SET 98: (SEQ ID No:233; SEQ ID No:234) ; SET 99: (SEQ ID No:235;  
15 SEQ ID No:236; SEQ ID No:237) ; SET 100: (SEQ ID No:238; SEQ ID  
No:239) ; SET 101: (SEQ ID No:240; SEQ ID No:241) ; SET 102: (SEQ  
ID No:242; SEQ ID No:243; SEQ ID No:244) ; SET 103: (SEQ ID  
No:245; SEQ ID No:246; SEQ ID No:247) ; SET 104: (SEQ ID No:248;  
SEQ ID No:249) ; SET 105: (SEQ ID No:250; SEQ ID No:251; SEQ ID  
20 No:252) ; SET 106: (SEQ ID No:253; SEQ ID No:254) ; SET 107: (SEQ  
ID No:255; SEQ ID No:256) ; SET 108: (SEQ ID No:257; SEQ ID  
No:258) ; SET 109: (SEQ ID No:259; SEQ ID No:260; SEQ ID No:261) ;  
SET 110: (SEQ ID No:262; SEQ ID No:200) ; SET 111: (SEQ ID No:263;  
SEQ ID No:264) ; SET 112: (SEQ ID No:265; SEQ ID No:266) ; SET  
25 113: (SEQ ID No:267; SEQ ID No:268) ; SET 114: (SEQ ID No:269; SEQ  
ID No:270) ; SET 115: (SEQ ID No:271; SEQ ID No:272) ; SET 116:  
(SEQ ID No:273; SEQ ID No:274) ; SET 117: (SEQ ID No:275; SEQ ID  
No:276) ; SET 118: (SEQ ID No:277; SEQ ID No:278) ; SET 119: (SEQ  
ID No:279; SEQ ID No:280; SEQ ID No:281) ; SET 120: (SEQ ID  
30 No:282; SEQ ID No:283; SEQ ID No:276) ; SET 121: (SEQ ID No:284;  
SEQ ID No:285) ; SET 122: (SEQ ID No:286; SEQ ID No:287; SEQ ID  
No:288) ; SET 123: (SEQ ID No:289; SEQ ID No:290) ; SET 124: (SEQ  
ID No:291; SEQ ID No:292) ; SET 125: (SEQ ID No:293; SEQ ID  
No:294; SEQ ID No:295) ; SET 126: (SEQ ID No:296; SEQ ID No:297) ;  
35 SET 127: (SEQ ID No:298; SEQ ID No:299; SEQ ID No:300) ; SET 128:  
(SEQ ID No:301; SEQ ID No:302; SEQ ID No:288) ; SET 129: (SEQ ID  
No:303; SEQ ID No:304) ; SET 130: (SEQ ID No:305; SEQ ID No:306;

SEQ ID No:307) ; SET 131: (SEQ ID No:308; SEQ ID No:309; SEQ ID  
No:310) ; SET 132: (SEQ ID No:311; SEQ ID No:312; SEQ ID No:313) ;  
SET 133: (SEQ ID No:314; SEQ ID No:315; SEQ ID No:316) ; SET 134:  
(SEQ ID No:317; SEQ ID No:318) ; SET 135: (SEQ ID No:319; SEQ ID  
5 No:320; SEQ ID No:321) ; SET 136: (SEQ ID No:322; SEQ ID No:323) ;  
SET 137: (SEQ ID No:324; SEQ ID No:325) ; SET 138: (SEQ ID No:326;  
SEQ ID No:327; SEQ ID No:328) ; SET 139: (SEQ ID No:329; SEQ ID  
No:330) ; SET 140: (SEQ ID No:331; SEQ ID No:332; SEQ ID No:333) ;  
SET 141: (SEQ ID No:334; SEQ ID No:335; SEQ ID No:336) ; SET 142:  
10 (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET 143: (SEQ ID  
No:339; SEQ ID No:340; SEQ ID No:341) ; SET 144: (SEQ ID No:342;  
SEQ ID No:343; SEQ ID No:344) ; SET 145: (SEQ ID No:345; SEQ ID  
No:346) ; SET 146: (SEQ ID No:347; SEQ ID No:348; SEQ ID No:349) ;  
SET 147: (SEQ ID No:350; SEQ ID No:351) ; SET 148: (SEQ ID No:352;  
15 SEQ ID No:353) ; SET 149: (SEQ ID No:354; SEQ ID No:355) ; SET  
150: (SEQ ID No:356; SEQ ID No:357) ; SET 151: (SEQ ID No:358; SEQ  
ID No:359; SEQ ID No:360) ; SET 152: (SEQ ID No:361; SEQ ID No:31)  
; SET 153: (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET  
154: (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET 155: (SEQ  
20 ID No:368; SEQ ID No:369; SEQ ID No:300) ; SET 156: (SEQ ID  
No:370; SEQ ID No:371) ; SET 157: (SEQ ID No:372; SEQ ID No:373;  
SEQ ID No:108) ; SET 158: (SEQ ID No:374; SEQ ID No:375; SEQ ID  
No:376) ; SET 159: (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ;  
SET 160: (SEQ ID No:380; SEQ ID No:381) ; SET 161: (SEQ ID No:382;  
25 SEQ ID No:383; SEQ ID No:384) ; SET 162: (SEQ ID No:385; SEQ ID  
No:386; SEQ ID No:387) ; SET 163: (SEQ ID No:388; SEQ ID No:389;  
SEQ ID No:390) ; SET 164: (SEQ ID No:391; SEQ ID No:392; SEQ ID  
No:393) ; SET 165: (SEQ ID No:394; SEQ ID No:395) ; SET 166: (SEQ  
ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET 167: (SEQ ID  
30 No:399; SEQ ID No:400; SEQ ID No:117) ; SET 168: (SEQ ID No:401) ;  
SET 169: (SEQ ID No:402; SEQ ID No:403) ; SET 170: (SEQ ID No:404;  
SEQ ID No:405; SEQ ID No:318) ; SET 171: (SEQ ID No:406; SEQ ID  
No:407; SEQ ID No:408) ; SET 172: (SEQ ID No:409; SEQ ID No:410;  
SEQ ID No:411) ; SET 173: (SEQ ID No:412; SEQ ID No:413) ; SET  
35 174: (SEQ ID No:414; SEQ ID No:415; SEQ ID No:416) ; SET 175: (SEQ  
ID No:417; SEQ ID No:418; SEQ ID No:419) ; SET 176: (SEQ ID  
No:420; SEQ ID No:421; SEQ ID No:422) ; SET 177: (SEQ ID No:423;

SEQ ID No:424; SEQ ID No:425) ; SET 178: (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET 179: (SEQ ID No:429; SEQ ID No:408) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ ID No:431) ; SET 182: (SEQ ID No:432) ; SET 183: (SEQ ID No:433; SEQ ID No:434) ; SET 184: (SEQ ID No:435; SEQ ID No:436) ; SET 185: (SEQ ID No:437) ; SET 186: (SEQ ID No:438; SEQ ID No:439) ; SET 187: (SEQ ID No:440; SEQ ID No:441) ; SET 188: (SEQ ID No:442) ; SET 189: (SEQ ID No:444) ; SET 190: (SEQ ID No:445) ; SET 191 (SEQ ID No:446 ; SEQ ID No:447) ; SET 192: (SEQ ID No:448) ; SET 193: (SEQ ID No:449) ; SET 194: (SEQ ID No:450) ; SET 195: (SEQ ID No:451) ; SET 196: (SEQ ID No:452) ; SET 197: (SEQ ID No:453) ; SET 198: (SEQ ID No:454) ; SET 199: (SEQ ID No:455) ; SET 200: (SEQ ID No:456) ; SET 201: (SEQ ID No:457) ; SET 202: (SEQ ID No:458) ; SET 203: (SEQ ID No:459) ; SET 204: (SEQ ID No:460) ; SET 205: (SEQ ID No:461) ; SET 206: (SEQ ID No:462) ; SET 207: (SEQ ID No:463) ; SET 208: (SEQ ID No:464) ; SET 209: (SEQ ID No:465) ; SET 210: (SEQ ID No:466) ; SET 211: (SEQ ID No:467) ; SET 212: (SEQ ID No:468)

3. A polynucleotide library according to Claim 2 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

4. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 1: (SEQ ID No:1 ; SEQ ID No:2) ; SET 4: (SEQ ID No:7 ; SEQ ID No:8) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 21: (SEQ ID No:46 ; SEQ ID No:47) ; SET 24: (SEQ ID No:54 ; SEQ ID No:55 ; SEQ ID No:56) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 38: (SEQ ID No:91 ; SEQ ID

No:92 ; SEQ ID No:93) ; SET 48: (SEQ ID No:115 ; SEQ ID No:116 ;  
SEQ ID No:117) ; SET 53: (SEQ ID No:126 ; SEQ ID No:127 ; SEQ ID  
No:128) ; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140)  
; SET 59: (SEQ ID No:141 ; SEQ ID No:142 ; SEQ ID No:143) ; SET  
5 61: (SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149) ; SET 64: (SEQ  
ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET 66: (SEQ ID  
No:162 ; SEQ ID No:163) ; SET 69: (SEQ ID No:168 ; SEQ ID No:169;  
SEQ ID No:170) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 85:  
(SEQ ID No:204; SEQ ID No:205) ; SET 88: (SEQ ID No:210; SEQ ID  
10 No:211) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 97: (SEQ ID  
No:230; SEQ ID No:231; SEQ ID No:232) ; SET 104: (SEQ ID No:248;  
SEQ ID No:249) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID  
No:252) ; SET 112: (SEQ ID No:265 ; SEQ ID No:266) ; SET 113: (SEQ  
ID No:267 ; SEQ ID No:268) ; SET 115 ; (SEQ ID No:271 ; SEQ ID  
15 No:272) ; SET 131: (SEQ ID No:308 ; SEQ ID No:309 ; SEQ ID No:310)  
; SET 132: (SEQ ID No:311 ; SEQ ID No:312 ; SEQ ID No:313) ; SET  
134: (SEQ ID No:317 ; SEQ ID No:318) ; SET 137: (SEQ ID No:324 ;  
SEQ ID No:325) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346) ; SET  
147: (SEQ ID No:350 ; SEQ ID No:351) ; SET 155: (SEQ ID No:368 ;  
20 SEQ ID No:369 ; SEQ ID No:300) ; SET 175: (SEQ ID No:417 ; SEQ ID  
No:418 ; SEQ ID No:419) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ  
ID No:431) ; SET 182: (SEQ ID No:432) ; SET 185: (SEQ ID No:437) ;  
SET 187: (SEQ ID No:440 ; SEQ ID No:441,

wherein said sequences are useful in  
25 differentiating a normal cell from a cancer cell.

5. A polynucleotide library according to Claim  
4 wherein said polynucleotide sequences or subsequences  
thereof of said pool correspond to any combination of at  
30 least one polynucleotide selected among those included in at  
least 50%, preferably 75% and more preferably 100% of the  
predefined sets.

6. A polynucleotide library according to Claim 4  
35 wherein the pool of polynucleotide sequences or subsequences



correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5           SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78)  
; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 131: (SEQ ID  
No:308 ; SEQ ID No:309 ; SEQ ID No:310) ; SET 145: (SEQ ID No:345  
; SEQ ID No:346) and SET 181: (SEQ ID No:431)

10           and of at least one polynucleotide sequence  
selected among those included in each one of predefined  
polynucleotide sequences sets comprising:

15           SET 38: (SEQ ID No:91 ; SEQ ID No:92 ; SEQ ID No:93)  
; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140); SET 61:  
(SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149); SET 69: (SEQ ID  
No:168 ; SEQ ID No:169 ; SEQ ID No:170) and SET 182: (SEQ ID  
No:432).

7     A polynucleotide library according to Claim  
6 wherein said polynucleotide sequences or subsequences  
thereof of said pool correspond to any combination of at  
20     least one polynucleotide selected among those included in at  
least 50%, preferably 75% and more preferably 100% of the  
predefined sets.

25     8. A library according to anyone Claim 1 or 2  
wherein the pool of polynucleotide sequences or subsequences  
correspond substantially to any combination of at least one  
polynucleotide sequence selected among those included in each  
one of predefined polynucleotide sequences sets comprising:

30           SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)  
; SET 26: (SEQ ID No:59; SEQ ID No:60 ; SEQ ID No:61) ; SET 32:  
(SEQ ID No:76; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID  
No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ  
ID No:99) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;SEQ ID No:137)  
; SET 64: (SEQ ID No:156 ; SEQ ID No:157; SEQ ID No:158) ; SET  
35     107: (SEQ ID No:255 ; SEQ ID No:256) ; SET 119: (SEQ ID No:279 ;

SEQ ID No:280 ; SEQ ID No:281) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ ID No:333) ; SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336) ; SET 145: (SEQ ID No:345; SEQ ID No:346) ; SET 148: (SEQ ID No:352; SEQ ID No:353) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162: (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET 165: (SEQ ID No:394 ; SEQ ID No:395) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416) and SET 188: (SEQ ID No:442),

wherein said sequences are useful in detecting a hormone sensitive tumor cell

9. A polynucleotide library according to Claim 8 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10. A library according to Claim 8 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346); SET 149: (SEQ ID No:354 ; SEQ ID No:355) and SET 169: (SEQ ID No:402 ; SEQ ID No:403)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99); SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137); SET 119: (SEQ ID

No:279; SEQ ID No:280 ; SEQ ID No:281) and SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416)

11. A polynucleotide library according to Claim 10 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

12. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 8: (SEQ ID No:16) ; SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 25: (SEQ ID No:57 ; SEQ ID No:58) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET 91: (SEQ ID No:216 ; SEQ ID No:217) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327 ; SEQ ID No:328) ; SET 139: (SEQ ID No:329 ; SEQ ID No:330) ; SET 141: (SEQ ID No:334 ; SEQ ID No:335 ; SEQ ID No:336) ; SET 158: (SEQ ID No:374 ; SEQ ID No:375 ; SEQ ID No:376) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 180: (SEQ ID No:430) and SET 186: (SEQ ID No:438 ; SEQ ID No:439),

wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

13. A polynucleotide library according to Claim 12 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

14. A library according to Claim 12 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136; SEQ ID No:137); SET 91: (SEQ ID No:216 ; SEQ ID No:217) and SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23; SEQ ID No:24) ; SET 40: (SEQ ID No:97; SEQ ID No:98 SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) and SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336).

15. A polynucleotide library according to Claim 14 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

16. A library according to anyone of Claims 1 or 2 wherein the pool of polynucleotide sequences or

subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5                   SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)  
; SET 22: (SEQ ID No:48 ; SEQ ID No:49 ; SEQ ID No:50) ; SET 23:  
(SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET 26: (SEQ ID  
10 No:59 ; SEQ ID No:60 ; SEQ ID No:61) ; SET 28: (SEQ ID No:65 ; SEQ  
ID No:66 ; SEQ ID No:67) ; SET 31: (SEQ ID No:73 ; SEQ ID No:74 ;  
SEQ ID No:75) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID  
No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 49: (SEQ ID  
No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;  
SEQ ID No:137) ; SET 64: (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID  
15 No:158) ; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 77: (SEQ ID  
No:186) ; SET 81: (SEQ ID No:194 ; SEQ ID No:195) ; SET 95: (SEQ  
ID No:226 ; SEQ ID No:227) ; SET 131: (SEQ ID No:308 ; SEQ ID  
No:309 ; SEQ ID No:310) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327  
; SEQ ID No:328) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ  
ID No:333) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162:  
20 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET 164: (SEQ ID  
No:391 ; SEQ ID No:392 ; SEQ ID No:393) ; SET 165: (SEQ ID No:394  
; SEQ ID No:395) and SET 183: (SEQ ID No:433 ; SEQ ID No:434),

                  wherein said sequences are useful in  
differentiating antracycline-sensitive tumors from  
25 antracycline-insensitive tumors.

17. A polynucleotide library according to Claim  
16 wherein said polynucleotide sequences or subsequences  
thereof of said pool correspond to any combination of at  
30 least one polynucleotide selected among those included in at  
least 50%, preferably 75% and more preferably 100% of the  
predefined sets.

18. A library according to Claim 16 wherein the  
35 pool of polynucleotide sequences or subsequences correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

5                   SET N° 32: (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78)  
; SET N°136: (SEQ ID No:322 ; SEQ ID No:323) ; SET N° 145: (SEQ ID  
No:345; SEQ ID No:346) ; SET N° 149: SEQ ID No:354; SEQ ID No:355)  
; SET N°169: (SEQ ID No:402 ; SEQ ID No:403)

10                   and of at least one polynucleotide sequence  
selected among those included in each one of predefined  
polynucleotide sequences sets comprising:

15                   SET No 11: (SEQ ID No:22; SEQ ID No:23 ; SEQ ID  
No:24); SET No 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ;  
SET No 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET  
No 119: (SEQ ID No:279 ; SEQ ID No:280 ; SEQ ID No:281) ; SET No  
174: (SEQ ID No:414 ; SEQ ID No:415; SEQ ID No:416).

20                   19. A polynucleotide library according to Claim  
18 wherein said polynucleotide sequences or subsequences  
thereof of said pool correspond to any combination of at  
least one polynucleotide selected among those included in at  
least 50%, preferably 75% and more preferably 100% of the  
predefined sets.

25                   20. A library according to anyone of Claims 1 or  
2 wherein the pool of polynucleotide sequences or  
subsequences correspond substantially to any combination of  
at least one polynucleotide sequence selected among those  
included in each one of predefined polynucleotide sequences  
sets comprising

30                   SET No 14 (SEQ ID No:30; SEQ ID No:31) ; SET No 23  
(SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET No 25 (SEQ ID  
No:57; SEQ ID No:58) ; SET No 27 (SEQ ID No:62; SEQ ID No:63; SEQ  
ID No:64) ; SET No 28 (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;  
SET No 32 (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET No 39  
35 (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET No 41 (SEQ ID

No:100; SEQ ID No:101; SEQ ID No:78) ; SET No 44 (SEQ ID No:106; SEQ ID No:107; SEQ ID No:108) ; SET No 48 (SEQ ID No:115; SEQ ID No:116; SEQ ID No:117) ; SET No 51 (SEQ ID No:122; SEQ ID No:78) ; SET No 64 (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET No 81 (SEQ ID No:194; SEQ ID No:195) ; SET No 83 (SEQ ID No:199; SEQ ID No:200) ; SET No 91 (SEQ ID No:216; SEQ ID No:217) ; SET No 96 (SEQ ID No:228; SEQ ID No:229) ; SET No 99 (SEQ ID No:235; SEQ ID No:236; SEQ ID No:237) ; SET No 108 (SEQ ID No:257; SEQ ID No:258) ; SET No 110 (SEQ ID No:262; SEQ ID No:200) ; SET No 116 (SEQ ID No:273; SEQ ID No:274) ; SET No 117 (SEQ ID No:275; SEQ ID No:276) ; SET No 118 (SEQ ID No:277; SEQ ID No:278) ; SET No 120 (SEQ ID No:282; SEQ ID No:283; SEQ ID No:276) ; SET No 126 (SEQ ID No:296; SEQ ID No:297;) ; SET No 142 (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET No 144 (SEQ ID No:342; SEQ ID No:343; SEQ ID No:344) ; SET No 149 (SEQ ID No:354; SEQ ID No:355) ; SET No 152 (SEQ ID No:361; SEQ ID No:31) ; SET No 153 (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET No 154 (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET No 157 (SEQ ID No:372; SEQ ID No:373; SEQ ID No:108) ; SET No 159 (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ; SET No 162 (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET No 166 (SEQ ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET No 167 (SEQ ID No:399; SEQ ID No:400; SEQ ID No:117) ; SET No 168 (SEQ ID No:401) ; SET No 171 (SEQ ID No:406; SEQ ID No:407; SEQ ID No:408) ; SET No 172 (SEQ ID No:409; SEQ ID No:410; SEQ ID No:411) ; SET No 173 (SEQ ID No:412; SEQ ID No:413) ; SET No 176 (SEQ ID No:420; SEQ ID No:421; SEQ ID No:422) ; SET No 177 (SEQ ID No:423; SEQ ID No:424; SEQ ID No:425) ; SET No 178 (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET No 179 (SEQ ID No:429; SEQ ID No:408) ; SET No 184 (SEQ ID No:435; SEQ ID No:436) ; SET No 185 (SEQ ID No:437),

wherein said sequences are useful in classifying good and poor prognosis primary breast tumors.

21. A polynucleotide library according to Claim 20 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at

least 50%, preferably 75% and more preferably 100% of the predefined sets.

22. A library according to Claim 20 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET N° 23 (SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET N° 25 (SEQ ID No:57 ; SEQ ID No:58) ; SET N° 32 (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET N° 41 (SEQ ID No:100 ; SEQ ID No:101 ; SEQ ID No:78) ; SET N° 48 (SEQ ID No:115 ; SEQ ID No:116 ; SEQ ID No:117) ; SET N° 51 (SEQ ID No:122 ; SEQ ID No:78) ; SET N° 64 (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET N° 81 (SEQ ID No:194 ; SEQ ID No:195) ; SET N° 83 (SEQ ID No:199 ; SEQ ID No:200) ; SET N° 91 (SEQ ID No:216 ; SEQ ID No:217) ; SET N° 99 (SEQ ID No:235 ; SEQ ID No:236 ; SEQ ID No:237) ; SET N° 110 (SEQ ID No:262 ; SEQ ID No:200) ; SET N° 116 (SEQ ID No:273 ; SEQ ID No:274) ; SET N° 142 (SEQ ID No:337 ; SEQ ID No:338 ; SEQ ID No:117) ; SET N° 144 (SEQ ID No:342 ; SEQ ID No:343 ; SEQ ID No:344) ; SET N° 149 (SEQ ID No:354 ; SEQ ID No:355) ; SET N° 162 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET N° 167 (SEQ ID No:399 ; SEQ ID No:400 ; SEQ ID No:117) ; SET N° 171 (SEQ ID No:406 ; SEQ ID No:407 ; SEQ ID No:408) ; SET N° 172 (SEQ ID No:409 ; SEQ ID No:410 ; SEQ ID No:411) ; SET N° 173 (SEQ ID No:412 ; SEQ ID No:413) ; SET N° 176 (SEQ ID No:420 ; SEQ ID No:421 ; SEQ ID No:422) ; SET N° 177 (SEQ ID No:423 ; SEQ ID No:424 ; SEQ ID No:425) ; SET N° 178 (SEQ ID No:426 ; SEQ ID No:427 ; SEQ ID No:428) ; SET N° 179 (SEQ ID No:429 ; SEQ ID No:408) ; SET N° 184 (SEQ ID No:435 ; SEQ ID No:436) ; SET N° 185 (SEQ ID No:437),

and at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET No 14 (SEQ ID No:30 ; SEQ ID No:31) ; SET No 27 (SEQ ID No:62 ; SEQ ID No:63 ; SEQ ID No:64) ; SET No 28 (SEQ ID



No:65 ; SEQ ID No:66 ; SEQ ID No:67) ; SET No 39 (SEQ ID No:94 ;  
SEQ ID No:95 ; SEQ ID No:96) ; SET No 44 (SEQ ID No:106 ; SEQ ID  
No:107 ; SEQ ID No:108) ; SET No 96 (SEQ ID No:228 ; SEQ ID  
No:229) ; SET No 108 (SEQ ID No:257 ; SEQ ID No:258) ; SET No 117  
5 (SEQ ID No:275 ; SEQ ID No:276) ; SET No 118 (SEQ ID No:277 ; SEQ  
ID No:278) ; SET No 120 (SEQ ID No:282 ; SEQ ID No:283 ; SEQ ID  
No:276) ; SET No 126 (SEQ ID No:296 ; SEQ ID No:297) ; SET No 152  
(SEQ ID No:361 ; SEQ ID No:31) ; SET No 153 (SEQ ID No:362 ; SEQ  
ID No:363 ; SEQ ID No:364) ; SET No 154 (SEQ ID No:365 ; SEQ ID  
10 No:366 ; SEQ ID No:367) ; SET No 157 (SEQ ID No:372 ; SEQ ID  
No:373 ; SEQ ID No:108) ; SET No 159 (SEQ ID No:377 ; SEQ ID  
No:378 ; SEQ ID No:379) ; SET No 166 (SEQ ID No:396 ; SEQ ID  
No:397 ; SEQ ID No:398) ; SET No 168 (SEQ ID No:401),

wherein the combination of overexpression of the  
15 genes identified by said first group of cluster sequences  
with the underexpression of the genes identified by said  
second group of cluster sequences are useful in classifying  
good and poor prognosis primary breast tumors.

20 23. A polynucleotide library according to Claim  
22 wherein said polynucleotide sequences or subsequences  
thereof of said pool correspond to any combination of at  
least one polynucleotide selected among those included in at  
least 50%, preferably 75% and more preferably 100% of the  
25 predefined sets.

24. A polynucleotide library according to anyone  
of Claims 1 to 23 wherein said tumor cells are breast tumor  
cells.

30 25. A polynucleotide library according to any of  
Claims 1 to 23 wherein said polynucleotides are immobilized  
on a solid support in order to form a polynucleotide array.

26. A polynucleotide library according to Claim 25 wherein the support is selected from the group comprising a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

5

27. A polynucleotide array useful for prognosis or diagnostic of tumor comprising an immobilized polynucleotide library according to Claims 1 to 3.

10

28. A polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of immobilized polynucleotide sequences sets according to claims 4 to 7.

15

29. A polynucleotide array useful to detect a hormone sensitive tumor cell comprising any combination of immobilized polynucleotide sequences sets according to claims 8 to 11.

20

30. A polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of immobilized polynucleotide sequences sets according to claims 12 to 15.

25

31. A polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors comprising any combination of immobilized polynucleotide sequences sets according to claims 16 to 19.

30

32. A polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any

combination of immobilized polynucleotide sequences sets according to claim 20 to 23.

5 33. A method of detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient and

10 b) reacting said polynucleotide sample obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any combination of the polynucleotide sequences of the polynucleotide library of Claims 1 to 23 or any combination of expression products encoded by any of the polynucleotide sequences of the  
15 libraries of Claims 1 to 23 and

c) detecting the reaction product of step (b).

20 34. A method for detecting differentially expressed polynucleotide sequences according to Claim 33 wherein said polynucleotide sample is labeled before its reaction step.

25 35. A method for detecting differentially expressed polynucleotide sequences according to Claim 34 wherein the label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent labels.

30 36. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 35 further comprising obtaining a control polynucleotide sample, reacting said control sample with said probe

detecting a control sample reaction product and comparing the amount of said polynucleotide sample reaction product to the amount of said control sample reaction product.

5                   37. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 36 wherein the polynucleotide sample is cDNA, RNA or mRNA.

10                   38. A method for detecting differentially expressed polynucleotide sequences according to Claim 37 wherein mRNA is isolated from said polynucleotide sample and cDNA is obtained by reverse transcription of said mRNA.

15                   39. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 38 wherein said reaction step is performed by hybridising the polynucleotide sample with the probe.

20                   40. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 39 wherein said method is used for detecting, diagnosing, staging, monitoring, predicting, preventing or treating conditions associated with cancer.

25                   41. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 40 wherein the cancer is breast cancer.

30                   42. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 41 wherein the product encoded by any of the polynucleotide sequences or polynucleotide sequences sets is involved in a receptor-ligand reaction on which detection is based.

43. A method for screening an anti-tumor agent comprising the method of Claim 33 wherein said polynucleotide sample is obtained from a patient treated with the anti-tumor agent to be screened.

Figure 1

## Normal Breast

Figure 1A

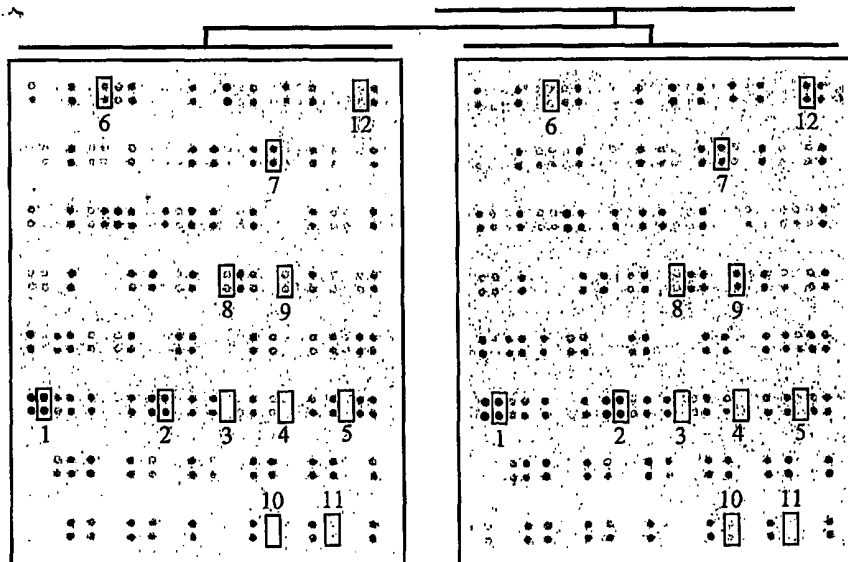
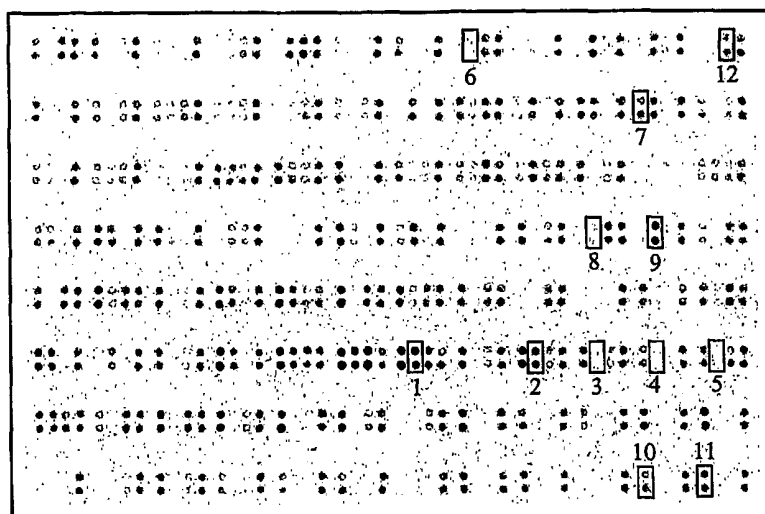


Figure 1B

ER-

ER+

Figure 1C

Breast cancer

Figure 2

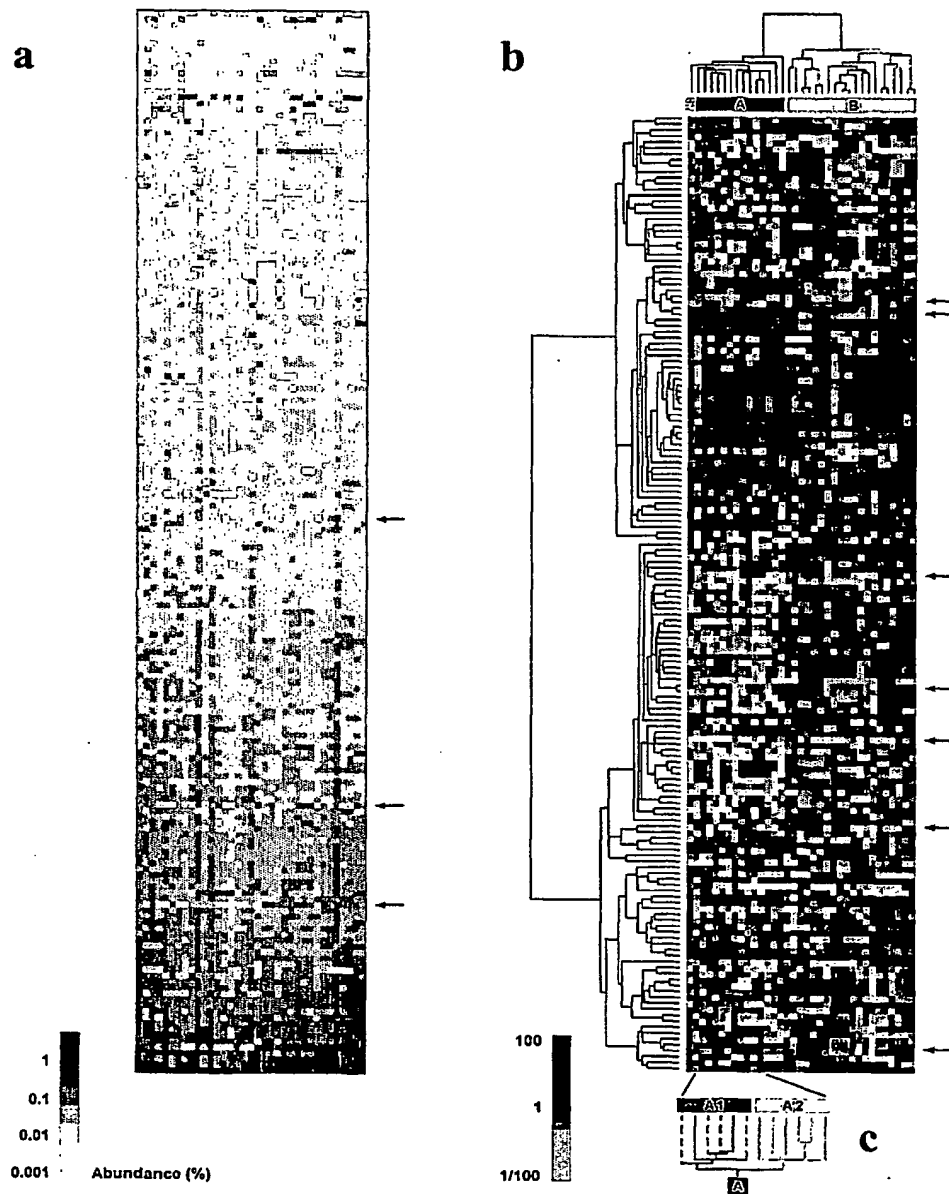


Figure 3

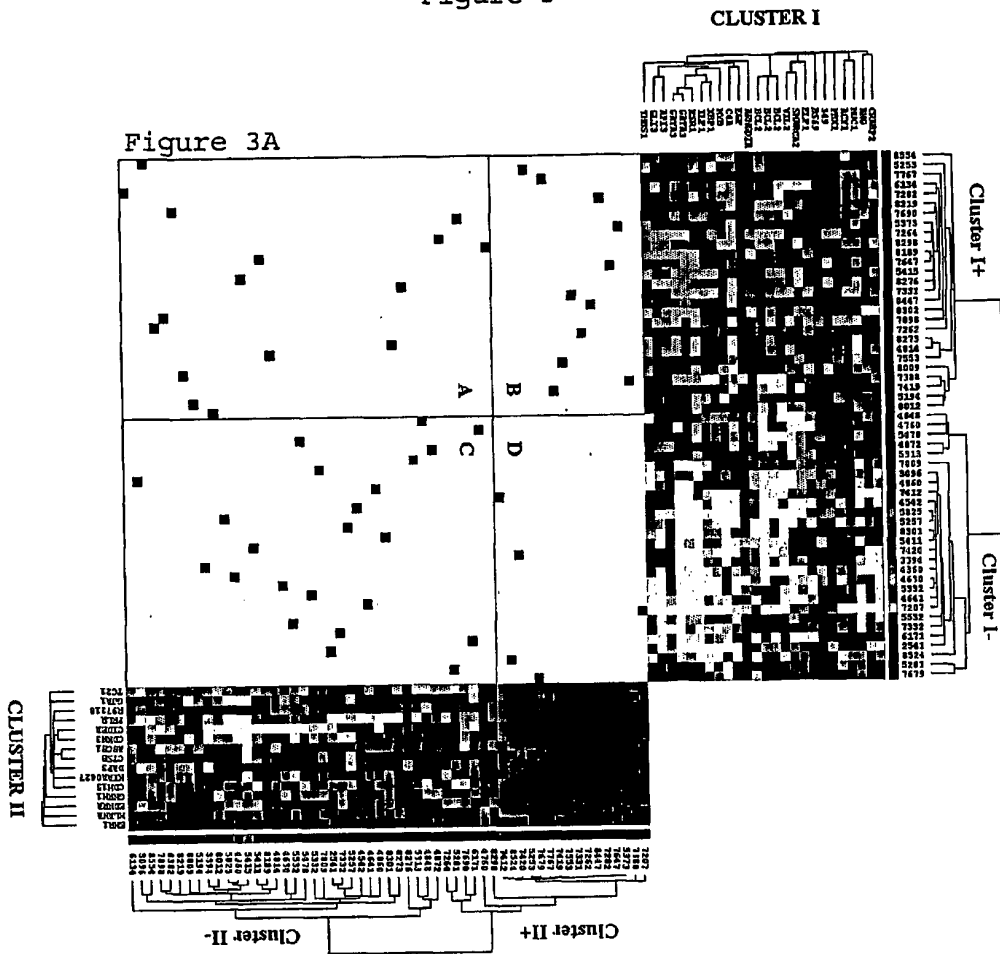


Figure 3C

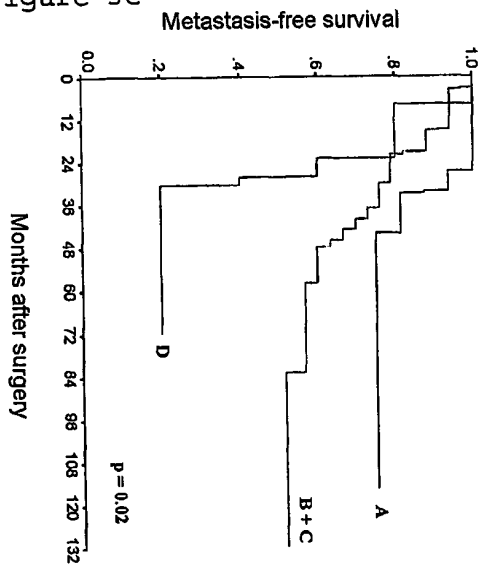


Figure 3B

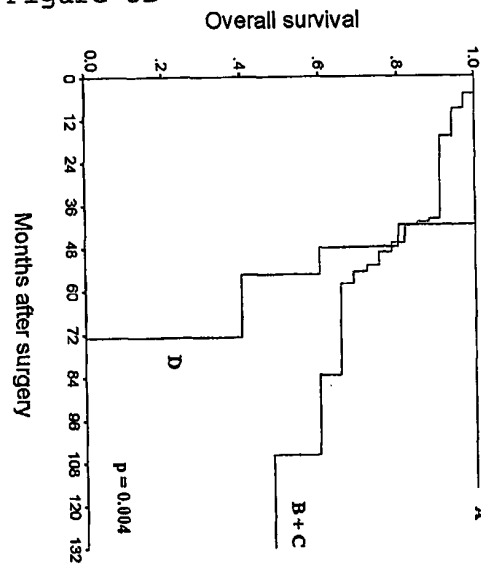




Figure 4

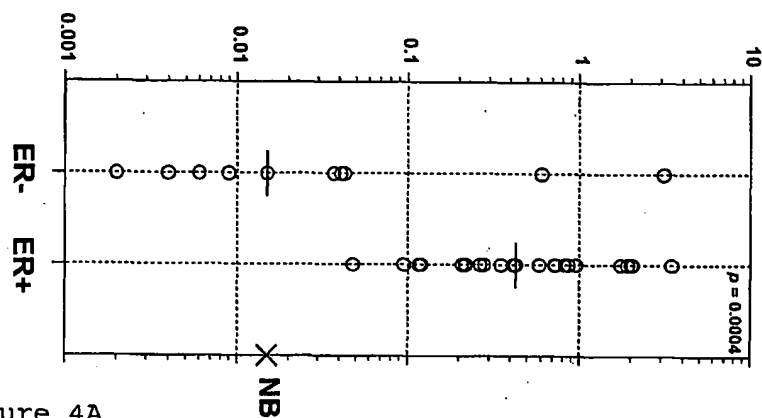


Figure 4A

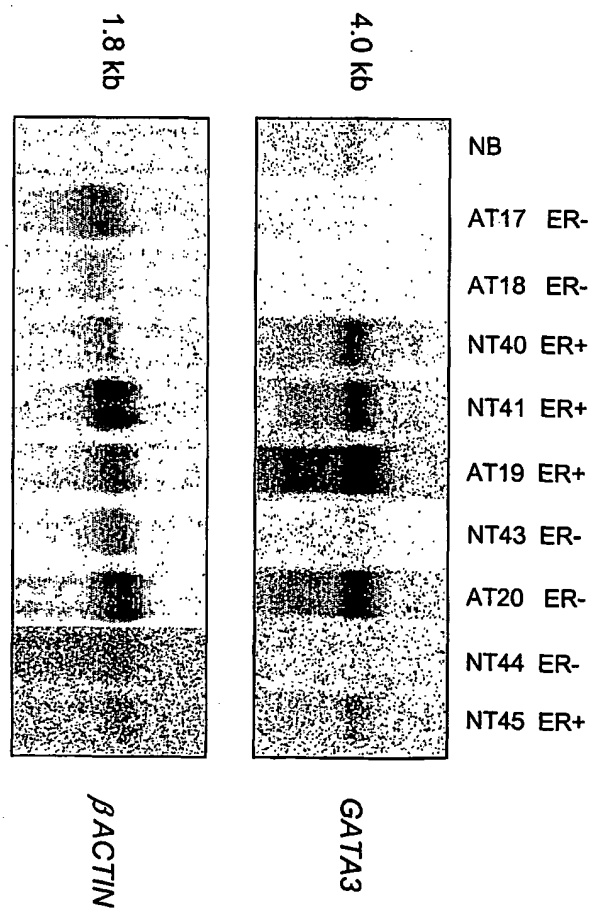


Figure 4B

## SEQUENCE LISTING

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<110> François Bertucci  
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tggcctgtga tccctacttg ttgcctcaca tccgaaagtc agtctctaca agtagccctg 2340
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gactccaagg ccacaaactg ttcaacacac acaaagtgga caaatggcgt tcagcagcgg 2460
gtttggaaca tagcgaatcc gaatggatct gatgaaacct gtaccaggtg cttttatttt 2520
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acaatttgaa cacttgacgg ttgtcccttt taattttatt gaagtgtat ttttttaaat 3300
aaaggttcat ctgtccatgc aaaaaaa 3327

```

&lt;210&gt; 7

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(300)

<223> 3' terminal sequence. ests, weakly similar  
to alu7\_human alu subfamily sq sequence  
contamination warning entry [h.sapiens] (EST  
T81919) gene.

&lt;400&gt; 7

```

tncaagagac aggggttnngc acattgccca ggatggtctc aaactcctag agttgagcta 60
tccacccacc tttggcctnc caaagtgtcg ggatcacagg cgtgagtcac tgtntccagc 120
accatcttgg aggtcttcta aagcccaggc cccacgccga gcttctgagt caataaagaa 180
gtctgcattt ctaacaagct tctaggggat gctgctgctg ctgctggtcc aggggcccga 240
ctttgaagaa ccactgcact gggtntttcc tctgggaccc gaatgcctgt gcttctcccc 300

```

&lt;210&gt; 8

&lt;211&gt; 369

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(369)  
<223> 5' terminal sequence. ests, weakly similar  
to alu7\_human alu subfamily sq sequence  
contamination warning entry [h.sapiens] (EST  
T81919) gene.

<400> 8  
cctaacgcag gtttccccgc aaatgactgg tcacgcggga ctgaacaccg cacaggcagg 60  
aggcatggca agggtaagtg aa ctgaagca ctttcaatac ttcctaccta accgcggggt 120  
ttccctccga gtaatgcgta aaatgggacc acgtggccca ctctgtttt tctctttggg 180  
ctctccacgt gccactcatg cttggaagag acagatttct ttctaggata aagatctctg 240  
ccccatttct gtcttttaaa atggagaatt ctttaaagaa gtagggacag cttncagggt 300  
cagggcagtt tgggaaagtn acaggggcct aattgtgttc cgtggaaacn ggggtaggag 360  
gtttgcttt 369

<210> 9  
<211> 255  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(255)  
<223> 3' terminal sequence. cyclin d1 (prad1:  
parathyroid adenomatosis 1) (CCND1) gene.

<400> 9  
aaagacagtt tttgggtaat cttttncttt tgcttaagtc agagatggaa gggggaaaga 60  
gcaaaggaaa aaacaaccaa caacaaggag aatgaagctt tcccttcttg tatcaaaatg 120  
ctccggagag gagggactnt cagtggagca cctggggccg gctccgcctc gctgcgggtg 180  
gcggtggcgc cctngcctg gcgccttcag atgtccacgt cccgcacgtc ggtgggtntg 240  
caagccaggt ccacc 255

<210> 10  
<211> 1325  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1325)  
<223> cyclin d1 (prad1: parathyroid adenomatosis  
1) (CCND1) gene.

<400> 10

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```
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gcgcgggggca gcagaagcga gagccgagcg cggacccagc caggaccac agccctcccc 120
agctgcccag gaagagcccc agccatggaa caccagctcc tgtgctgcga agtggaaacc 180
atccgccgag cgtaccccga tgccaacctc ctcaacgacc ggggtgctgcg ggccatgctg 240
aaggccgagg agacctgcgc gccctcgggtg tcctacttca aatgtgtgca gaaggaggtc 300
ctgccgtcca tgcggaagat cgtcgccacc tggatgctgg aggtctgcga ggaacagaag 360
tgcgaggagg aggtcttccc gctggccatg aactacctgg accgcttct gtcgctggag 420
cccgtgaaaa agagccgcct gcagctgctg ggggccactt gcatgttcgt ggcctctaag 480
atgaaggaga ccatccccct gacggccgag aagctgtgca tctacaccga cggctccatc 540
cggcccgagg agctgctgca aatggagctg ctcttggtga acaagctcaa gtggaacctg 600
gccgcaatga cccgcacga ttctattgaa cacttcctct ccaaaatgcc agaggcggag 660
gagaacaaac agatcatocg caaacacg cg cagaccttcg ttgcctcttg tgccacagat 720
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gccctgctgg agtcaagcct gcgccaggcc cagcagaaca tggaccccaa ggccgccgag 960
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tgacttaagc aaaagaaaaa gattacccaa aaactgtctt taaaagagag agagagaaaa 1260
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
aaaaa 1325
```

&lt;210&gt; 11

&lt;211&gt; 449

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(449)

<223> 5' terminal sequence. signal transducer and  
activator of transcription 1, 91kd (STAT1) gene.

&lt;400&gt; 11

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ttaggaagtt caacatcttg ggcacgcaca caaaagtgat gaacatggag gagtccacca 120
atggcagctc ggcggtgtaa tttcggcacc tgcaattgaa agaacaga aa aatgctggca 180
ccagaacgaa tgagggtcct ctcatcgta ctgaagagct tcaactccctt agttttgaaa 240
cccaattgtg ccagcctggg tttggttaatt gacctcgaga cgacctctct gcccgttgtg 300
ggtgatctcc aacgtcagcc agctcccag cggttggggc ctccattcct ttgggtacaa 360
catgctgggt nggcgggaac ccgggg antc tgttcttnt ttcctggact ccaccatgtg 420
ncacgggtggg gtttcagntt ttcagaagt 449
```

&lt;210&gt; 12

&lt;211&gt; 4003

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4003)



<223> signal transducer and activator of  
transcription 1, 91kd (STAT1) gene.

<400> 12

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gccatcctcg agagctgtct aggttaacgt tcgcactctg tgtatataac ctgcacagtc 120
ttggcaccta acgtgctgtg cgtagctgct cctttggttg aatccccagg cccttggttg 180
ggcacaaagg gcgagagatg ctgagtggtg cgaacttcag cagcttgact caaaattcct 240
ggagcaggtt caccagcttt atgatgacag ttttcccatg gaaatcagac agtacctggc 300
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ccgttttcat gacctcctgt cacagctgga tgatcaatat agtcgctttt ctttgagaa 420
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tctgaaaaac ccccagagat ttaat caggc tcagtcgggg aatattcaga gcacagtgt 600
gttagacaaa cagaaagagc ttgacagtaa agtcagaaat gtgaaggaca aggttatgtg 660
tatagagcat gaaatcaaga gcctggaaga tttacaagat gaatatgact tcaaatgcaa 720
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gtagataaac tcagaaattt aattcatgtt tcttaaatgg gctactttgt cctttttgtt 3360
attaggggtg tatttagtct att agccaca aaattgggaa aggagtagaa aaagcagtaa 3420

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ctgacaactt gaataatata ccagagataa tatgagaatc agatcatttc aaaactcatt 3480
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gcgaatgggt ccattctctc tcctgtactt ttccagaca cttttttgag tggatgatgt 36 00
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&lt;210&gt; 13

&lt;211&gt; 167

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(167)

&lt;223&gt; 3' terminal sequence. fibroblast growth

factor receptor 2 (bacteria -expressed kinase,  
keratinocyte growth factor receptor, craniofacial  
dysostosis 1, crouzon syndrome, pfeiffer syndrome,  
jackson-weiss syndrome) (FGFR2) gene.

&lt;400&gt; 13

```

ccacctctgc tcggtgaaaa ttaagaaatt atgtgtaaga acagcattta gcaaatagct 60
attaaaaaaa gagagaccaa ttttctag gt gcattgggac atccatttaa antcaatata 120
aaaaataact ccttgtaaatt ntataatata ttatttatac ntaattt 167

```

&lt;210&gt; 14

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(414)

&lt;223&gt; 5' terminal sequence. fibroblast growth

factor receptor 2 (bacteria -expressed kinase,  
keratinocyte growth factor receptor, craniofacial  
dysostosis 1, crouzon syndrome, pfeiffer syndrome,  
jackson-weiss syndrome) (FGFR2) gene.

&lt;400&gt; 14

```

ggacacagaa tggataagcc agccaactgc accaacgaac tgtacatgat gatgaggagac 60
tgttggcatg cagtgcctcc cagagaccaa cgttcaagca gttggtagaa gacttggatc 120
gaattctcac tctcacaacc aatgaggaaat acttggacct cagccaacct ctogaacagt 180
attcacctag ttaccctgac ac aagaagtt cttgttcttc aggagatgat tctgtttttt 240
ctccagaccc catgccttac gaaccatgcc ttctcagta tccacacata aacgggcagt 300
gttttaaaac atgaatgact gtgtctggcc tgncccaa acagggacag gcaactggggg 360
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<210> 15  
<211> 4667  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(4667)  
<223> fibroblast growth factor receptor 2  
(bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson -weiss syndrome) (FGFR2) gene.

<400> 15  
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gggggccccg aggcgcgcgc ttgcctgcgc gctctgagcc ttgcgaactc gcgagcaaag 180  
tttggtggag gcaacgccaa gcctgagtc tttcttctc tcgttcccc aatccgaggg 240  
cagcccgccg gcgtcatgcc cgcgctctc cgcagcctgg ggtacgcgct gaagcccggg 300  
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gcggaggagc gttgccattc aagtactgc agcagcagcg gcagcgctc ggttcctgag 480  
cccaccgcag gctgaaggca ttgcgcgtag tccatgccc tagaggaagt g tgcagatg 540  
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gctggggctg tttcatctgc ctggtcgtg tcaccatggc aaccttgctc ctggcccggc 660  
cctcctcag tttagttag gataccacat tagagccaga agagccacca accaaatacc 720  
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gcctctatgc ttgtactgcc agtagactg tagacagtga aacttggtac ttcattggtga 960  
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aacgtatccc cctgcggaga caggtttcgg ctgagtcag ctctccatg aactccaaca 1920  
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caaaattgga gaaagtattt aataaaacct gtttaatttt atactgacaa taaaaatgtt 4620
totacagata ttaatgttaa caagaca aaa taaatgtcac gcaactt 4667

```

&lt;210&gt; 16

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(483)

<223> 3' terminal sequence. ests (EST T89980)  
gene.

&lt;400&gt; 16

```

gtgttgagct cccaaaaggc ttaaaacttg ctttgtgaat gaatgatctt aaatcactag 60
tgaagatgat catggggcat ttgcacatta aagaactaaa atgaaatgaa aaagccatga 120
ctcctcactt aatgctatta aaaaaaaatc tgatttggtg aattaacccc acttctcata 180
gtttaatttg gtaatcaacg ttcttgggaa ttc aggttct catgggcacc ctaatagtgt 240
ttagggccgg ggttctgag gctgctggg gtgatccga ggaacaagaa gctgccctat 300
taaaagtaat ctacttgagt ttttcccgag tcttgggag ttgttcccta ctgtggggct 360
acttataggg tagggcccc ccaaatccct cacacttagg tcggccctgc tggttgcgtg 420
tggggctctg aaangcagcc gctaggangt cccaagcct naacttacc attttctggc 480

```

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ctg

483

<210> 17  
<211> 400  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(400)  
<223> 3' terminal sequence. protein phosphatase 3  
(formerly 2b), catalytic subunit, gamma isoform  
(calcineurin a gamma) (PPP3CC) gene.

<400> 17  
ntttatatat attgaacata aattaaaaga atttataaaa cagccacctt tttacagaat 60  
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tttccaataa taaataaata gaatttgttc ttgagtttta gatccacctg agccacggca 180  
ggactctaag tcatgaatgg gctttcttcc cttgggtcgt cctgtgcgca gatgntgagt 240  
gtgctgaggt tacagatttc attggcccac cagcgtgtat gc tatecttt cgggggtggg 300  
cattcgctca ttaattcggg cccagncct cgcgctttct ttcaaaactc cgggatcttg 360  
tgcntggagg cgaggnaccc ctctgatggg cttcccgagg 400

<210> 18  
<211> 490  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(490)  
<223> 5' terminal sequence. protein phosphatase 3  
(formerly 2b), catalytic subunit, gamma isoform  
(calcineurin a gamma) (PPP3CC) gene.

<400> 18  
cttggagcac tatacccaca aactgtccg aggggtgctct tatttctaca gttaccctgc 60  
agtttgtgaa tttttgcaga acaataattt actatcaatt atcagagccc atgaagccca 120  
agatgctggg tatcgaatgt acaggaagag ccaagccaca ggttttccat cacttattac 180  
aattttctct gcccacaatt acctagatgt ctataacaat aaagctgctg tgttgaaata 240  
tgaaaacaat gtcataata tcaggcagtt taactgttct ccacaccct actgggcttc 300  
caaactttat gggatgtttt cacatgggtc ttgacctttt gttgggggga ccccgacac 360  
agaggatggc tgggtaaatg tggntcaaca ttatggntct ggatggacgg aactgatttt 420  
ctggatggat ggaagcngga tgggaaggca cttacngttt cgtaaggng g ttcttcggg 480  
gnntaggttc 490

<210> 19  
<211> 2134  
<212> DNA/RNA  
<213> Artificial Sequence

<220>

13/292

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2134)

<223> protein phosphatase 3 (formerly 2b),  
catalytic subunit, gamma isoform (calcineurin a  
gamma) (PPP3CC) gene.

&lt;400&gt; 19

```
gggccaccct tagcagcgggt cgcggtcgggt gccgaagcgg tgttccccgc cttagccgct 60
gcgcctccca agagagcggc cggtagggccc tcgtcctgtc agtggcgctc gaggc cggcc 120
tgcggtggcc gcgcccttct ggtgctcgga caccgctgag gagccggggc cgggcacggc 180
tggctgacgg ctccgggcag ctaaggctgc ccgaggagaa ggccggcgcc gcggcgtagg 240
cgcacgtccg gcgggctcct ggagcctgga ggagccgag gggacatgt ccgggaggcg 300
cttcacctc tccaccaccg accgcgtcat caa agctgtc ccccttcctc caacccaacg 360
gottactttc aaggaagtat ttgagaatgg gaaacctaaa gttgatgttt taaaaaacca 420
tttggtaaag gaaggacgac tggaagagga agtagcctta aagataatca atgatggggc 480
tgccatcctg aggcaagaga agactatgat agaagtagat gctccaatca cagtatgtgg 540
tgatattcat ggacaattct ttgacctaat gaagttattt gaagttggag gatcacctag 600
taacacacgc tacctctttc tgggtgacta tgtggacaga ggctatttca gtatagagtg 660
tgtgctgtat ttatggagtt taaagattaa tcatoccaaa acattgtttc tgcttcgggg 720
aatcatgaa tgcaggcatc ttacagacta tttcaccttc aaacaggaat gtc gaatcaa 780
atatcggaa caggtgtatg atgcctgtat ggagacattt gactgtcttc ctctgtctgc 840
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agatgacatt aggaaattag acaggtttac ggaacctccc gcctttggac ctgtgtgtga 960
cctgctttgg tctgatccct cagaggatta t ggcaatgag aagacctgg agcactatac 1020
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gcagaacaat aatttactat caattatcag agcccatgaa gccaagatg ctgggtatcg 1140
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caattaccta gatgtctata acaataaagc tgctgtgttg aaatatgaaa acaatgtcat 1260
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gcgaatgcc accccgaaag atagcatata ccttggtggg ccaatgaaat ctgtaacctc 1740
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aaaaagtga tctgttttgt tttcccttt tttctccata attttaagaa atgaatctga 2040
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gccttgga a cctcaaacct gggtttctga cccc 2134
```

&lt;210&gt; 20

&lt;211&gt; 248

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(248)

<223> 3' terminal sequence. ests (EST T90726)  
gene.

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&lt;400&gt; 20

atccatttat tatatccaat gctaaacact accacttgga ctctaagata tgtttatgcc 60  
tctctgttta ttctagtttt ttaaaaatca aatatacaag atctacaatt atttatatcc 120  
aagatgtcta caccactgcc taagaagcta ttaaaatat t tgtatttggtg caatgggnacc 180  
cattattcac atgggcctag gattaaaaag tcaatttata ttngngaataa atttntccaa 240  
aaaaacca 248

&lt;210&gt; 21

&lt;211&gt; 427

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(427)

<223> 5' terminal sequence. ests (EST T90726)  
gene.

&lt;400&gt; 21

taagatacga acgagaaacc tgatttattg ctcaccttc ccttgccctcc ctaatggcaa 60  
gcaaaactct gaacatctga aaaggatgta gttctggaca aatcct gact acccagagga 120  
aactcactgt gagattgctg ttgatttgaa ggggtgcttc actaaggta tattttaag 180  
tagaataaca catgctgagt gtaaaactggg ctttgattg gtcagctgca gtagtacaaa 240  
aacagcatag aatttgagga aaactaaaac tgctatgaga taggctatga ggaaaactta 300  
aaactggcta tgtggttagga aatg atgtta aanttatgtg gggaaagttt ttcccctccn 360  
tattacttca cattacaggc ctttngaggg gcntctgggc tctgnaccn gtttgatggg 420  
cctttga 427

&lt;210&gt; 22

&lt;211&gt; 294

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(294)

<223> 3' terminal sequence. sry (sex determining  
region y)-box 4 (SOX4) gene.

&lt;400&gt; 22

tttcttggtt ttcttttttt ttttccgaaa ccaactgccc tccactgact gcccctgtac 60  
cacatcaaac agtctcctct cctccacgcc tccggggtct ggaagtctc acctcactga 120  
tttcacgtag aaaagaaggc ggaggccagc agccgcgcgc ncaagctccc caacgtgcaa 180  
atccatttca gtttgaccgt gaacccctt ccagttcgtg tcctcctccg cccccgcccc 240  
tagtccccgc tgctggnctt caacggggtt ntccgggtcat ttctagcgc cgg 294

&lt;210&gt; 23

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(362)

&lt;223&gt; 5' terminal sequence. sry (sex determining region y)-box 4 (SOX4) gene.

&lt;400&gt; 23

```
ttccggactt gtctgcaccc ccagcaagaa ggcgagttag ttttctagag acttgaagga 60
gtctccccct tctgcatca ccaccttgggt ttgttttat ttgtcttctt ggtcaagaaa 120
ggaggggaga acccagcgca ccctccccct ctttttttaa acgctgatg aagacagaag 180
gtccgggggt gacgaatttg gccgatggag nat gtttttg gggaacgccg ggactgagag 240
actccacggc agggcgaaatt ccggtttggg gctttttttt tctccctct tttccctt 300
gcccttttg canccgngg agggagntgt tnaagggag ggagggccag ccagtgttga 360
cc 362
```

&lt;210&gt; 24

&lt;211&gt; 2797

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2797)

&lt;223&gt; sry (sex determining region y) -box 4 (SOX4) gene.

&lt;400&gt; 24

```
ttccccagca ttcgagaac tctctctac tttagcacgg tctccagact cagccgagag 60
acagcaaaact gcagcgcggt gagagagcga gagagaggga gagagagact ctccagcctg 120
ggaactataa ctctctctcg agaggcggag aactccttcc ccaaactctt tggggacttt 180
tctctcttta ccacctccg ccctgcgag gatttgagg gccagttcg ccgccgcgcg 240
cgtcttcccg ttcggcgtgt gcttgcccg gggaaccggg agggcccgcc gatcgcgcg 300
cggccgcgcg gaggtgtga gcgcgcgtg gcgccgcgcg agccgagggc atggtgcagc 360
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ccggcctcga gctgggaate gcctcctccc caacgcccg ctccaccgcc tccacgggcg 480
gcaaggccga cgaccggagc tgggtcaaga ccccgagtgg gcacatcaag cgacctatga 540
acgccttcat ggtgtggtcg cagatcgagc ggcgcaagat catggagcag tcgcccga 600
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acctgctcga cctgaacccc agctcaaaact ttgagagcat gtccctgggc agcttcagtt 1620
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cgctcgctggc gctcgaccgg gacctggatt ttaacttcga gcccggtcc ggctcgact 1680
tcgagttccc ggactactgc acgcccagg tgagcgagat gatctcgga gactggctcg 1740
agtccagcat ctccaacctg gttttcacct actgaa gggc gcgcaggcag ggagaagggc 1800
cggggggggt aggagaggag aaaaaaaaag tgaaaaaaag aaacgaaaag gacagacgaa 1860
gagtttaaaag agaaaaggga aaaaagaaag aaaaagtaag cagggtcgt tcgcccgcgt 1920
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cgaactgga gggggttcac ggtcaaaactg aaatggattt gcacgttggg gagctggcg 264 0
cggcggctgc tgggcctcg cttcttttc tacgtgaaat cagtgggtg agacttcca 2700
gaccccgag gcgtggagga gagagactg tttgatgtg tacaggggca gtcagtggag 2760
ggcgagtgtt ttcgaaaaa aaaaagaaa aaaagg 2797

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&lt;210&gt; 25

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(352)

&lt;223&gt; 5' terminal sequence. ring finger protein 5 (RNF5) gene.

&lt;400&gt; 25

```

acggggggcc caacnanant cgcgagcngg gcgtggcggg cgcgaccttc gaatgt anta 60
tatgtttgga gactgctcgg gaagctgttg tcagtgtgtg tggccacctg tactgttggc 120
catgtcttca tcagtggctg gagacacggc cagaacggca agagtgtcca gtatgtaaag 180
ctgggatcag cagagagaag gttgtccgc ttatggggc agggagccag aagccccagg 240
atcccagatt aaaaactcca cccgccccc aggcc agaga ccagctccg agagcagagg 300
gggattccag ccatttggtg ataccggggg cttccacttn ttcatttggg gt 352

```

&lt;210&gt; 26

&lt;211&gt; 543

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(543)

&lt;223&gt; ring finger protein 5 (RNF5) gene.

&lt;400&gt; 26

```

atggcagcag cggaggagga ggacgggggc cccgaagggc caaatcgca gcggggcggg 60
gcgggcgcga cttogaatg taatatatgt ttggagactg ctcggaagc tgtgtcagt 120

```

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gtgtgtggcc acctgtactg ttggccatgt cttcatcagt ggctggagac acggc cagaa 180
cggcaagagt gtccagtatg taaagctggg atcagcagag agaaggttgt cccgctttat 240
gggagaggga gccagaagcc ccaggatccc agattaaaaa ctccaccccg cccccagggc 300
cagagaccag ctccggagag cagaggggga ttccagccat ttggtgatac cgggggcttc 360
cactttcat ttggtgttgg tgcttttccc ttt ggctttt tcaccaccgt ctccaatgcc 420
catgagcctt tccgcggggg tacaggtgtg gatctgggac agggtcaccc agcctccagc 480
tggcaggatt ccctcttcct gtttctcgcc atcttcttct ttttttggt gctcagtatt 540
tga 543

```

&lt;210&gt; 27

&lt;211&gt; 397

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(397)

<223> 3' terminal sequence. axl receptor tyrosine  
kinase (AXL) gene.

&lt;400&gt; 27

```

gccgtggggt gggaaagtgg gaag gtggag ttttcccag tggcagtgt tagcttggat 60
cctgagaggg agtaccaggt ggaggggtgt ctcaggcacc atcctcctgc cctgggctgc 120
tggggagccc ctatcagcag gctgagcggg gctaggggtt ttggaagggc agaggacata 180
gcntccagca ggtggacct cagccgcagt naggcagcta caggaatcct tagggtctgg 240
ctgggttggg gggtcagctc ctctgcagc tccaggggnt tcaggataac ctccaccctc 300
atccatnttn acatagagga tttcgtcagg ctctgggggc aggangcaan gcctttcagt 360
ntgttctcca aatcttccn caactctnta aaacttt 397

```

&lt;210&gt; 28

&lt;211&gt; 418

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(418)

<223> 5' terminal sequence. axl receptor tyrosine  
kinase (AXL) gene.

&lt;400&gt; 28

```

ctgaatgaga acatgtccgt gtgtgtggcg gacttcgggc tctccaagaa gatctaca at 60
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agtctagctg accgtgtcta caccagcaag agcgatgtgt ggtccttcgg ggtgacaatg 180
tgggagattg ccacaagagg ccaaaccoca tatccggggc gtggagaaca gcgagattta 240
tgantatctg cgccagggaa atcgctgaa gcagcct ncg gactgtcttg gatgggantg 300
ttatgccttg atgttcggg tncctgggga gcttaaattc cccaggggnc ccgnccaatt 360
ttttacaaag cttnccggga agatttttgg gagnacacac ttttaagggc tttncctt 418

```

&lt;210&gt; 29

&lt;211&gt; 5015

&lt;212&gt; DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(5015)

<223> axl receptor tyrosine kinase (AXL) gene.

<400> 29

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ccagatagag agacacggcc tctactggctc agcaccaggg tccccctccc cctcctcagc 120
tccctcctcg gcccttttaa gaaagagctg atcctctcct ctcttgagtt aaccctgat 180
tgtccagggtg gcccttggt ctggcctggg gggcggaggc aaagggggag ccaggggagg 240
agaaaagggt gcccaagtct gggagtgagg gaaggaggca ggggtgctga gaaggcggct 300
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gatgggcagg gtcccgcctg cctggtgctt ggctgtgtgc ggctgggctg gcatggcccc 540
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ccggggactc acgggcaccc ttcggtgtca gctccagggt cagggagagc ccccgagggt 660
acattggctt cgggatggac agatcctgga gctcgcggac agcaccaga cccagggtgc 720
cctgggtgag gatgaacagg atgactggat agtggtcagc cagctcag aa tcacctccct 780
gcagctttcc gacacgggac agtaccagtg tttgggtgtt ctgggacatc agacctctgt 840
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caggactgtg gccgccaaca ccccttcaa cctgagctgc caagctcagg gacccccaga 960
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tggagctgtg atggaaggcc agctcaacca ggacgactcc atcctcaagg tggctgtgaa 2160
gacgatgaag attgccatct gcacgaggtc agagctggag gatttctga gtgaagcggg 2220
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gaaggccttg cctcctgccc aggagcctga cgaaatcctc tatgtcaaca tggat gaggg 2940
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```

19/292

```

ccctaaggat tccctgtagct gcctcactgc ggctgaggct catcctgctg gacgctatgt 3060
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```

&lt;210&gt; 30

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(439)

<223> 5' terminal sequence. cathepsin b (CTSB)  
gene.

&lt;400&gt; 30

```

aacacgtcac cggagagatg atgggtggcc atgcatccgc atcctgggct ggggagtgga 60
gaatggcaca ccctactggc tgg ttgcaa ctcctggaac actgactggg gtgacaatgg 120
cttcttttaa atactcagag gacaggatca ctgtggaac gaatcagaag tgggtggctgg 180
aattccacgc accgatcagt actgggaaaa gatctaattc gccgtgggcc tgtcgtgcca 240
gtcctggggg gcgagatcgg ggtagaaatg cattttatc ttttaagttc cgtaaggat 300
acaagtttcc agacagggtc tgaaagggan tgggatttng gccaaacatc agacctgttc 360
tttcccaagg gaggaccaag ttctgggct aacattcccc agcctnttgg ttttaacagt 420
gncaggacag ggcntgtt 439

```

20/292

<210> 31  
<211> 1996  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1996)  
<223> cathepsin b (CTSB) gene.

<400> 31  
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ctgggctggg gtgcagtggg gcgaccacg g ctcacggcag cctcagccac ccagatgtaa 120  
gcatctggg tcccacctca gctcccagag tagtgatctc aggatccggc ttccaacatg 180  
tggcagctct gggcctccct ctgctgcctg ctggtgttg ccaatgcccg gagcaggccc 240  
tctttccatc ccctgtcgga tgagctggtc aactatgtca acaaacggaa taccacgtgg 300  
caggccgggc acaacttcta caacgtggac atgagctact tgaagaggct atgtggtacc 360  
ttcctgggtg ggcccaagcc accccagaga gttatgttta ccgaggacct gaagctgcct 420  
gcaagcttcg atgcacggga acaatggcca cagtgtccca ccatcaaaga gatcagagac 480  
cagggtcctc gtggctcctg ctgggccttc ggggctgtgg aagccatct c tgaccggatc 540  
tgcatccaca ccaatgcgca cgtcagcgtg gaggtgtcgg cggaggacct gctcacatgc 600  
tgtggcagca tgtgtgggga cggctgtaat ggtggctatc ctgctgaagc ttggaacttc 660  
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tactccatcc ctccctgtga gcaccac gtc aacggctccc ggcccccatg cacgggggag 780  
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gagatctaca aaaacggccc cgtggaggga gctttctctg tgtattcgga ctccctgctc 960  
tacaagtcag gagtgtacca acacgtcacc ggagagatga tgggtggcca tgccatccgc 1020  
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ctgaccact gatctctact accacaagga aaatagttta ggagaaacca gcttttactg 1920  
tttttgaaaa attacagctt caccctgtca agttaacaag gaatgcctgt gccataaaaa 1980  
ggtttctcca acttga 1996

<210> 32  
<211> 492  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(492)

21/292

<223> 3' terminal sequence. protein phosphatase 4  
(formerly x), catalytic subunit (PPP4C) gene.

<400> 32

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aacaacagaga aaaaagaagg aaaaaaagaa aaaaaaatta ttggaaactt catggttcaa 120
gtggggagag aggaggagga acatggagct aggtctccag gcctctccag agaagtcctc 180
accctcgaag caccctcttg ggggacagca gagccagg ga cagccccccc ccacgcccag 240
cctccgtctg agggaagatg ggcagagtca cagtgggtgc gaggggccag aagggttggg 300
aggngggcag gggcgggcgg ggtcacagga agtagttcgg ccacggcttt ctttgggagg 360
gggatncccc gtgtcttctt ttgggggagc agccttcaaa gatgatgaaa tctttttctt 420
gggagatgct tcgttc cagc ttnccaagat tggttncca cattttccca cagcgggtaca 480
agttagtttt tg 492
```

<210> 33

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(330)

<223> 5' terminal sequence. protein phosphatase 4  
(formerly x), catalytic subunit (PPP4C) gene.

<400> 33

```
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ctggcactta aggttcgcta tcctgatcgc atcacactga tccgggg caa ccatgagagt 120
cgccagatca cgcaggctta tggcttctac gatgagtgcc tgcgcaagta acggctcggg 180
gactgtgtgg cgctactgca ctgagatctt tgactacctc agcctgtcag ccatcatcga 240
tngaaagaat cttctgcgtg caggggggcc tctccccctc catccagacc ctgggatcca 300
gattcggaca atcgaccgaa agcaa gaggt 330
```

<210> 34

<211> 1429

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(1429)

<223> protein phosphatase 4 (formerly x),  
catalytic subunit (PPP4C) gene.

<400> 34

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gagggggcgg cggcccccgc tctgaccgc gccgggggtg ggccatggcg gagatcagcg 120
acctggaccg gcagatcgag cagctgcgtc gctgcgagct catcaaggag agcgaagtca 180
aggccctgtg cgctaaggcc agagagatct tggtagagga gagcaacgtg cagaggggtg 240
actcgccagt cacagtgtgc ggcgacatcc atggacaatt ctatgacctc aaagagctgt 300
tcagagtagg tggcgacgtc cctgagacca actacctctt catggggggac tttgtggacc 360
gtggttctta tagcgtcgaa acgttcctcc tgctgctggc acttaaggt t cgctatcctg 420
atcgcatcac actgatccgg ggcaaccatg agagtcgcca gatcacgcag gtctatggct 480
```

22/292

```

tctacgatga gtgcctgcgc aagtacgggt cggtagactgt gtggcgctac tgcactgaga 540
tctttgacta cctcagcctg tcagccatca tcgatggcaa gatcttctgc gtgcacgggg 600
gcctctcccc ctccatccag accctgg atc agattcggac aatcgaccga aagcaagagg 660
tgcctcatga tgggcccattg tgtgacctcc tctggtctga cccagaagac accacaggct 720
ggggcgtgag cccccgagga gccggctacc tatttggcag tgacgtggtg gccagttca 780
acgcagccaa tgacattgac atgatctgcc gtgcccacca actggtgatg gaaggttaca 840
agtggcactt caatgagacg gtgctcactg tgtggtcggc acccaactac tgctaccgct 900
gtgggaatgt ggcagccatc ttggagctgg acgagcatct ccagaaagat ttcacatct 960
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tttcttctt ttttctgtt gtttttagat aaaaatttt agaaaaaaa tgaaaaaatt 1320
ctaataaaag aagaaaaatg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1380
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1429

```

&lt;210&gt; 35

&lt;211&gt; 493

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(493)

<223> 3' terminal sequence. ests (EST T79867)  
gene.

&lt;400&gt; 35

```

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tcccttcccc aagctagctt tggaa taaat ccacttttct tgtaccagac cccactcttg 120
ttaattggac tctacatgtg gnaagcaact aacttgattt tcggttacaa tataatattc 180
aacttcagta aatcaaagac aattttgaaa gaagccaaag ggaaaaaaat gacctgaaga 240
gtcctgttta anttagatt tctgaacaca aatctctggc gactaggact gaagcttgac 300
ctnttcttac ccaggaccn ttcccacctc actagggnac tttggantgg gatatatgtg 360
gggaaactct tgggctttcc ccattgtggc accatttcat atcttatggc aaatggtgcc 420
tcctacctcc ctgggncac tcccngttg gatgggtntt gggggaggag nctgntggg 480
gntttttccc at 493

```

&lt;210&gt; 36

&lt;211&gt; 354

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(354)

<223> 3' terminal sequence. fibroblast growth  
factor receptor 4 (FGFR4) g ene.

&lt;400&gt; 36

```

ttttgtttt ttatttcaaa aaaataattt ataaaacgcc atttgctcct gttttcggca 60
ggcttccagc ttctctgggc tcaggggcaa tgctcccgtc aagacgtgg ggcagcagca 120

```

23/292

```
gcagggggag gtnctgggaa aggggggttca gagggccaga acctcctgct ggtattggga 180
ggcaggaggt ttagcatagc agctctcca g ccaggctcag ccaaaccgg gatggggact 240
aagcgccaag gtccaagaag ccgagcagaa ccctgacatt tggggccatc aggacanagg 300
cacggcagct cccaaggga aggggcacgg ccttngggac angggcacag caac 354
```

&lt;210&gt; 37

&lt;211&gt; 336

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(336)

<223> 5' terminal sequence. fibroblast growth  
factor receptor 4 (FGFR4) gene.

&lt;400&gt; 37

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ggcagcagcg ccctccaga ggcctacott caagcagctg gtggaggcgc tggacaagg 120
ctgctggccg tctctgagga gtacctcgac ctccgcctga ccttcggacc ctattcccc 180
tctggtgggg aacgccagca gcacctgctt cctccagcga ttctgtcttc agccacgacc 240
ccctgccatt ggggattcag ctcttcctt ttgggtctng ggggtgcagac atga gcaagg 300
ctnaagggtt ttgcaaggga catagggttg gtgggc 336
```

&lt;210&gt; 38

&lt;211&gt; 3015

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3015)

<223> fibroblast growth factor receptor 4 (FGFR4)  
gene.

&lt;400&gt; 38

```
ccgaggagcg ctcgggctgt ctgcggaccc tgccgcgtgc aggggtcgcg gccggctgga 60
gctgggagtg aggcggcgga ggagccaggt gaggaggagc caggaaggca gttggtggga 120
agtccagctt gggccctga gagctgtgag aaggagatgc ggctgctgct gg ccctgttg 180
ggggtcctgc tgagtgtgcc tgggctoca gtctgtccc tggaggcctc tgaggaagtg 240
gagcttgagc cctgcctggc tcccagcctg gacgagcaag agcaggagct gacagtagcc 300
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gagggcagtc gcctggcacc tgctggcgt gtacggggct ggaggggccc cctagagatt 420
gccagcttcc tacctgagga tgctggcgc tacctctgcc tggcacgagg ctccatgac 480
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gaccccaagt cccataggga cctctcgaat aggcacagtt acccccagca agcaccctac 600
tgagacacacc ccagcgcat ggagaagaaa ctgcatgcag tacctgcggg gaacaccgtc 660
aagttccgct gtccagctgc aggcaacccc acgcccacca tccgctggct taaggatgga 720
caggccttcc atggggagaa ccgcattgga ggcattcggc tgcgccatca gcaactggag 780
ctcgtgatgg agagcgtggt gccctcgac cgcggcacat acacctgcct ggtagagaac 840
gctgtgggca gcatccgcta taactacctg ctagatgtgc tggagcggtc cccgcaccgg 900
cccatcctgc aggcggggt cccggccaac accacagccg tgggtggcag cgacgtggag 960
ctgctgtgca aggtgtacag cgatgcccag cccacatcc agtggctgaa gcacatcgtc 1020
```



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```

atcaacggca gcagcttcgg agccgacg gt ttccctatg tgcaagtcct aaagactgca 1080
gacatcaata gctcagaggt ggaggtcctg tacctgcgga acgtgtcagc cgaggacgca 1140
ggcgagtaca cctgcctcgc aggcaattcc atcggcctct cctaccagtc tgcctggctc 1200
acggtgctgc cagaggagga cccacatgg accgcagcag cgcggcaggc caggataacg 1260
gacatcatcc tgtacgcgtc gggctccctg gccttggtg tgcctctgct gctggccggg 1320
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agctcatccc tggtagcagg cgtgcgtctc tccctcagcg g ccccgctt gctcgccggc 1500
ctcgtgagtc tagatctacc tctcgacca ctatgggagt tccccggga caggctggtg 1560
cttggaagc ccctaggcga gggctgcttt ggccaggtag tacgtgcaga ggcctttggc 1620
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gcctctgaca aggacc tggc cgacctggtc tcggagatgg aggtgatgaa gctgatcggc 1740
cgacacaaga acatcatcaa cctgcttggg gtctgcacc aggaagggcc cctgtacgtg 1800
atcgtggagt gcgcgcgcaa gggaaacctg cgggagttcc tgcgggccc ggcggcccca 1860
ggcccgacc tcagcccgga cgttccctcg agcagtggg ggcgcgtctc ctcc cagtc 1920
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atccaccggg acctggctgc ccgcaatgtg ctggtgactg aggacaatgt gatgaagatt 2040
gctgactttg ggctggccc cggcgctccac cacattgact actataagaa aaccagcaac 2100
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cagagtgcag tgtggtcttt tgggatcctg ctatgggaga tcttcaccct cgggggctcc 2220
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gctgctatgc taaacctcct gcctcccaat accagcagga ggttctggc ctctgaacc 2880
cctttcccca cactcccc tgctgctgct gccccagcgt cttgacggga gcattggccc 2940
ctgagcccag agaagctgga agcctgccga aaacaggagc aaatggcgtt ttataaa tta 3000
tttttttgaa ataaa 3015

```

&lt;210&gt; 39

&lt;211&gt; 252

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(252)

<223> 3' terminal sequence. ectonucleotide  
pyrophosphatase/phosphodiesterase 2 (autotaxin)  
(ENPP2) gene.

&lt;400&gt; 39

```

gtgtgattta ttatgtttta gattggttta taaggcttaa atatatctgt catagttaac 60
agttaacagc aaataaaggc aactttacaa aatcagtgtt tccatacagt acaggactaa 120
atgtggcaac tgtgcattgg aaaattaata ttctctaat gcaaatntca aatctgcagc 180
accatttaga agcttcact aaaaactcaa gctgcagtat ttattacang ctctactcng 240
aacacanggc ta 252

```

&lt;210&gt; 40

&lt;211&gt; 382

25/292

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(382)

<223> 5' terminal sequence. ectonucleotide  
pyrophosphatase/phosphodiesterase 2 (autotaxin)  
(ENPP2) gene.

&lt;400&gt; 40

```
ctnacnttca aacgganntg gaa ttatttc caaagggtat tggatgaagaa atatgcttcg 60
gaaagaaatg gagttaacgt gataagtggg ccaatcttcg actatgacta tgatggctta 120
catgacacag aagacaaaat aaaacagtac gtggaaggca gttccattcc tgttccaact 180
cactactaca gcatcatcac cagctgtctg gattttactc agcctgccga caagtgtgac 240
ggccctctct ctgtgtcttc ctcatcctg cctcaccggc ctgacaacga ggagagctgc 300
aatagctcag aggacgnatt caaatgggt agnaggaact catgaaggnt gcacacagct 360
agggtncgtt gacctttgna cc                                     382
```

&lt;210&gt; 41

&lt;211&gt; 2592

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2592)

<223> ectonucleotide  
pyrophosphatase/phosphodiesterase 2 (autotaxin)  
(ENPP2) gene.

&lt;400&gt; 41

```
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ggagtcataa tctgcttagg attcactgca catcgaatta agagagcaga aggatgggag 120
gaaggtcctc ctacagtgtc atcagactcc ccctggacca acatctccgg atcttgcaag 180
ggcaggtgct ttgaaactca agaggctgga cctcctgatt gtcgctgtga caacttgtgt 240
aagagctata ccagttgtct ccatgacttt gatgagctgt gtttgaagac agcccgctgc 300
tgaggagtga ctaaggacag atgtggggaa gtcagaaatg aagaaaatgc ctgtcactgc 360
tcagaggact gcttgccag gggagactgc tgtaccaatt accaagtggg ttgcaaagga 420
gagtcgcatt gggttgatga tgactgtgag gaaataaagg ccgcagaatg ccc tgcaggg 480
tttgttcgcc ctccattaat catcttctcc gtggatggct tccgtgcac ataatgaag 540
aaaggcagca aagtcatgcc taatattgaa aaactaaggc ctgtgtggac acactctccc 600
tacctgaggg cgggtgtacc aactaaaacc ttctctaact tatacacttt ggccactggg 660
ctatatccag aatcacatgg aattgttggc a attcaatgt atgacctgt atttgatgcc 720
acttttcatc tgcgagggcg agagaaatth aatcatagat ggtggggagg tcaaccgcta 780
tggtattacag ccaccaagca aggggtgaaa gctggaacat tcttttggtc tgttgtcatc 840
cctcacgagc ggagaatatt aaccatattg cagtggctca ccctgccaga tcatgagagg 900
ccttcggtct atgccttcta ttctgagcaa cctgatttct ctggacacaa atatggccct 960
ttcggccctg agatgacaaa tcctctgagg gaaatcgaca aaattgtggg gcaattaatg 1020
gatgactaga aacaactaaa actgcatcgg tgtgtcaacg tcatctttgt cggagaccat 1080
ggaatggaag atgtcacatg tgatagaact gagttcttga gtaattacct aactaatgtg 1140
gatgatatta ctttagtgcc tggaactcta ggaagaattc gatccaaatt tagcaacaat 1200
gctaaatatg accccaaagc cattattgcc aatctcacgt gtaaaaaacc agatcagcac 1260
tttaagcctt acttgaaaca gcacctccc aaacgtttgc actatgccaa caacagaaga 1320
```

26/292

```

attgaggata tccatttatt ggtg gaacgc agatggcatg ttgcaaggaa acctttggat 1380
gtttataaga aaccatcagg aaaatgcttt ttccaggag accacggatt tgataacaag 1440
gtcaacagca tgcagactgt tttttaggt tatggcccaa catttaagta caagactaaa 1500
gtgcctccat ttgaaaacat tgaactttac aatgttatgt gtgatctcct gggattgaag 156 0
ccagctccta ataatgggac ccatggaagt ttgaatcatc tcctgcgcac taataccttc 1620
aggccaacca tgccagagga agttaccaga cccaattatc cagggattat gtaccttcag 1680
tctgattttg acctgggctg cacttgtgat gataaggtag agccaaagaa caagttggat 1740
gaactcaaca aacggcttca taaaaaggg tctacaga ag agagacacct cctctatggg 1800
cgacctgcag tgctttatcg gactagatat gatattttat atcacactga ctttgaaagt 1860
ggttatagtg aaatattcct aatgccactc tggacatcat atactgtttc caaacaggct 1920
gaggtttcca gcgttcctga ccatctgacc agttgcgtcc ggctgatgt ccgtgtttct 1980
ccgagtttca gt cagaactg tttggcctac aaaaatgata agcagatgtc ctacggattc 2040
ctctttcctc cttatctgag ctcttcacca gaggtctaat atgatgcatt ccttgtaacc 2100
aatatggttc caatgtatcc tgctttcaaa cgggtctgga attatttcca aagggtattg 2160
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aagatgcaca cagctagggt gcgtgacatt gaacatctca ccagcctgga cttcttccga 2520
aagaccagcc gcagctaccc agaaatcctg aactcaaga catacctgca tacatatgag 2580
agcgagattt aa 2592

```

&lt;210&gt; 42

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(467)

<223> 3' terminal sequence. v-rel avian  
reticuloendotheliosis viral oncogene homolog a  
(nuclear factor of kappa light polypeptide gene  
enhancer in b-cells 3 (p65)) (RELA) gene.

&lt;400&gt; 42

```

acagatttat tagttcagag tagaaagagc aagagtccaa gtgctttgat tgttcagtaa 60
aaactatgcc tcnagactgg agagctgcca gcctgctctc cccactctt aacaacttac 120
cctactatta aggcaactga gaagagggag agcaaggaag tcccagacca aacccttct 180
ggatccnggg ngagagccag tgctgttgcn tggtnntcct tcagccatgg ttgagcaagg 240
aaagagccgg cagagacctc ttagaggcag gaaggccagc ccctcaaacg ctggtnttag 300
ggcacagggg acaatgccag tgccatacag gggctggtat ctgggggcgt tattttgatt 360
aagctgtaat gaatccatga tgggaaggac acttgataag gctttntggg gctcaaaggn 420
ctttacctcc agcctgcttc tntctctagg gngagtaccc agaagct 467

```

&lt;210&gt; 43

&lt;211&gt; 2444

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

27/292

&lt;222&gt; (1)..(2444)

<223> v-rel avian reticuloendotheliosis viral  
oncogene homolog a (nuclear factor of kappa light  
polypeptide gene enhancer in b-cells 3 (p65))  
(RELA) gene.

&lt;400&gt; 43

```
ggcaacgaggc ggggccgggt cgcagctggg cccgcggcat ggacgaactg ttccccctca 60
tcttcccggc agagcagccc aagcagcggg gcatgcgctt ccgctacaag tgcgaggggc 120
gtcccgcggg cagcatccca ggcgagagga gcacagatac caccaagacc caccaccacca 180
tcaagatcaa tggctacaca ggaccaggga cagtgcgcat ctccctggtc a ccaaggacc 240
ctcctcaccg gcctcaccoc cagcagcttg taggaaagga ctgccgggat ggcttctatg 300
aggctgagct ctgcccggac cgctgcatcc acagtttcca gaacctggga atccagtgtg 360
tgaagaagcg ggacctggag caggctatca gtcagcgcac ccagaccaac aacaaccctt 420
tccaagttcc tatagaagag cagcgtgggg actacgacct gaatgctgtg cggctctgct 480
tccaggtgac agtgcgggac ccatcaggca ggccccctcg cctgccgcct gtcctttctc 540
atcccatctt tgacaatcgt gcccccaaca ctgccgagct caagatctgc cgagtgaacc 600
gaaactcttg cagctgcctc ggtggggatg agatcttctt actgtgtgac aagggtgcaga 660
aagaggacat tgaggtgtat ttacggggac caggctggga ggcccgaggc tccttttcgc 720
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ctgtgttcac agacctggca tccgtcgaca actccgagtt tcagcagctg ctgaaccagg 1440
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caggaggcat agtttttagt gaacaatcaa agcacttgga ctcttgcctt ttctactctg 2400
aactaataaa gctgttgcca agctggacgg cagcagctcg tgcc 2444
```

&lt;210&gt; 44

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(381)

28/292

<223> 5' terminal sequence. il2 -inducible t-cell  
kinase (ITK) gene.

<400> 44

```
aactctttcc tttggttggtg ctaagaggtg atgcccaagg tgcaccacct ttcaagaact 60
ggatcatgaa caactttatc ctcttggaag aacagctcat caagaaatcc caacaagaga 120
agaacttctc cctcgaactt taaagtccgc ttctttgtgt taaccaaagc cagcctgg ca 180
tactttgaag atcgtcatgg gaagaagcgc acgctgaagg ggtccattga gctctcccga 240
attcaaagtgt gttgaggttg tgaaaagtga catcagcatc ccatgccact attaaatacc 300
cgttttcagg tnggtgcatg acaacttacc tcctnttatg gtgtttgntt ccagntcgtg 360
aggaggccgg ncagcgttng g                                     381
```

<210> 45

<211> 6381

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(6381)

<223> il2-inducible t-cell kinase (ITK) gene.

<400> 45

```
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attcagatat gtttgaaaca ttcttaaggc tacaaaacag aacatagaaa aataaacagg 120
aatatattca acacttacaa aaagtgatat gataaagaat ataaagtact agtttccttt 180
taacacttca aaagatatgt atatatactt ttttttacaa gtaacatcac aaatgctcac 240
atcttcacat gctcttaaag tattatttgt actcagtgtg aggctattat cgtttttcat 300
acataaaatt ttctagctct gtaacacaat gcaattttta atccattcag taagttcaac 360
cccaaagttg ccgcttccca gcattaagac atgcacccac ccctcttcta agattttcta 420
aacttgtatt tcggggagaa agacctct tt taaaaaataa tccaattagt gggagagtaa 480
atggctgaca ttagtagcaa aaccttagtt atctgaaaat aacatattgg aaatgagaca 540
ttattaggat tttaaacaaa caatagcatt tagacataaa gtaggaagca aaatacagta 600
aacagaaata gtgtagccaa atatcattct cttcagctac ctttaagtaa agacaaaaca 660
tttacctcat ctaaaaatga aggtaaaacg aaagaggcaa aaataaatat tgctagtttc 720
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tcaatcataa gcaagtgttc agttcacagg cattttaatt caaccttgag tcacaaagga 840
gaacaacacg ctgcgagaa acagtctaca gtctgcatta aataagaa ta tatcagcatt 900
gtggtctggg aaaacctatg cttgccagga caaggcaggg tgctgagctt aggtcatgcc 960
atgaaaatga atttgtgggt tatcagtaaa cagtatgagg actacacaga tgccagcatc 1020
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acaacaccaa aggaaaaggg ggct ggaatc aagttcagcc aaagcaccta acacaaaaaa 1140
caggtgagct ttggtcagtc tgtcttcaa aatatgtatg atcatatggt aatgaagttt 1200
cataatttcc aactcaaaaa tacaaatgat cctcagttct atacttttgc ctctattctc 1260
ttataaagaa atatgtcaac ataacagtat gacataacag ttaaaataag gacaaaagct 132 0
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ctacataaaa aagcatgagc tgaaagtggg ggacctcta tcttctcatt ccttaactga 1860
gccaccgatg ttaagaaaaa aatggcttaa gcggtacctt caacaactat tctagttaag 1920
aaggtgacaa caaattgagg ccgcgaattc ggcgaaaact ctttcctttg g ttgtgctaa 1980
gaggtgatgc ccaaggtgca ccacctttca agaactggat catgaacaac tttatcctcc 2040
```

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30/292

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&lt;211&gt; 274

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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&lt;220&gt;

&lt;221&gt; misc\_feature

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&lt;223&gt; 5' terminal sequence. tenascin xb (TNXB) gene.

&lt;400&gt; 46

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&lt;211&gt; 13268

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

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&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

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&lt;223&gt; tenascin xb (TNXB) gene.

&lt;400&gt; 47

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gtaccggg 13268

```

&lt;210&gt; 48

&lt;211&gt; 438

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(438)

&lt;223&gt; 3' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

&lt;400&gt; 48

```

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tagatattta aatgacttta tataaaataa ttcaccactt ccaagtataa aaacaaaatc 120
tcacagtgcg tgancaatgt cctctc ttga cttctcagag aacagaaggg gttcctgagc 180
aggtagcctg gggggacacc agaggngcct ctggggctcc tcctgctctg atgccaccaa 240
gtgctcaaaa agagcttctg cagtggggtt gggattgctt ttttgacctt taaaatatta 300
tatgtttaag gtaggggggg atgaaggggg gaatgccctt tttatttttc ttcccatttt 360
aaaaatatgt gttttctagg catccaaata tagggggctg tggcctggga gggctaggcc 420
ccctttgccca ggttcact 438

```

&lt;210&gt; 49

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(390)

<223> 5' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 49

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ctggggctga gcaggttatc cctgtcagga gccctgggac tgggctgcat ctacagccca 180
cctggcatgg taccagctc ccatccactt cttcaccctt ctttcctcct gacctgggt 240
caacagtgat ggacctcca actcttcacc caccctctt accattcacc tctaaaccag 300
gggaagccag gggtngggag agcant cagg gagagccagg gcttcagttt tccaattgct 360
ggggangggc ttccattttn tggggccagg 390
```

<210> 50

<211> 2475

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2475)

<223> colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 50

```
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caccacagcga gcgagcgagc gagcgagggc ggccgacgcg cccggccggg acccagctgc 120
ccgtatgacc gcgcggggcg ccgcggggcg ctgccctccc acgacatggc tgggctccct 180
gctgttggtg gtctgtctcc tggcgagcag gactatcacc gaggaggtgt cggagtactg 240
tagccacatg attgggagtg gacacctgca gtctctgcag cggtgattg acagtcagat 300
ggagacctcg tgccaaatta catttgagtt tgtagaccag gaacagttga aagatccagt 36 0
gtgctacctt aagaaggcat ttctcctggt acaagacata atggaggaca ccatgcgctt 420
cagagataac acccccaatg ccatcgccat tgtgcagctg caggaaactct ctttgaggct 480
gaagagctgc ttcaccaagg attatgaaga gcatgacaag gcctgcgtcc gaactttcta 540
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```

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```

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tatcaatttg cactt                                     2475

```

&lt;210&gt; 51

&lt;211&gt; 397

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(397)

<223> 3' terminal sequence. villin 2 (ezrin)  
(VIL2) gene.

&lt;400&gt; 51

```

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catagcatta tctttgagca tcccacgggtg ttccgcatgc cacacctgga tccggtcctc 120
ccactggctc ctggttaagtt tgtgtggtc catcactctt tgagggatca nccgctcaga 180
gctgaggtag ccagacttgt gcacttcttt gttgtagtc ccaaacttgg cctgcacagc 240
gtagggaccc caagagcacg gcagtctcag ggggggcagt agatctcatc gctaagggat 300
tcctttcctt cacttnggag ggaggaaaag tttctgggt gatgtcctgg ggatgagctt 360
ccttcagcca catctttcag ggnaggact ttnggcc                                     397

```

&lt;210&gt; 52

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(468)

<223> 5' terminal sequence. villin 2 (ezrin)  
(VIL2) gene.

&lt;400&gt; 52

```

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tccagccaaa tacaactgga aaacagcttt ttgatcaggt ggtaaagact atcggcctcc 240
gggaagtgtg gtactttggc ctccactatg tggatnaata aaggatttcc tacctgg gct 300
gaagctggat aagaaggtgt ctgcccagga ggtcaggaag gagaatcccc tccagttcaa 360

```

37/292

gttccggggc caagttctac cctgaagatg tgggtgagg agctcattcc agggacattc 420  
accagaaat tttttttcnt ccaagtgaag gaagggattc ttaggcgn 468

&lt;210&gt; 53

&lt;211&gt; 3064

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3064)

&lt;223&gt; villin 2 (ezrin) (VIL2) gene.

&lt;400&gt; 53

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```

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aaaa
3064

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&lt;210&gt; 54

&lt;211&gt; 435

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(435)

&lt;223&gt; 3' terminal sequence. adenomatosis polyposis coli (APC) gene.

&lt;400&gt; 54

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&lt;210&gt; 55

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(414)

&lt;223&gt; 5' terminal sequence. adenomatosis polyposis coli (APC) gene.

&lt;400&gt; 55

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&lt;210&gt; 56

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<220>  
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<223> adenomatosis polyposis coli (APC) gene.

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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence:primer

<220>  
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<220>  
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tcttacacaa acccagcagt ggcag ccaact tctgccaaact tgtaggggca cgtcgccctc 1620
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&lt;210&gt; 59

&lt;211&gt; 359

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(359)

&lt;223&gt; 3' terminal sequence. insulin-like growth factor 2 (somatomedin a) (IGF2) gene.

&lt;400&gt; 59

```

ttagccaatt gatttttttg gtggttggtt tttttaaagc caatttctga gcttttgtgg 6 0
ggtgtttcta aaaagccaat tagttttaag aggggtgttg tggggggggg ggaagggggg 120
tagtttaatg ttttgatttt ttatgtgttg ggataatttg ggataatttg gggggagggt 180
atgtgaaggg tgtttaaagc caatcgattt tgtacatgtt tgaagatgct gctgtgcttc 240
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&lt;210&gt; 60

&lt;211&gt; 410

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(410)

&lt;223&gt; 5' terminal sequence. insulin-like growth factor 2 (somatomedin a) (IGF2) gene.

&lt;400&gt; 60

```

gtcgaccct cggaccgtgc ttccggacaa cttcccaga taccctgtgg gcaagttctt 60
ccaatatgac acctgggaag cagtcacacc agcgctgca ggggcnctgc ctgccctcct 120
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<210> 61  
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<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1356)  
<223> insulin-like growth factor 2 (somatomedin a)  
(IGF2) gene.

<400> 61  
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<210> 62  
<211> 474  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(474)  
<223> 3' terminal sequence. egf-like module  
containing, mucin-like, hormone receptor-like  
sequence 1 (EMR1) gene.

<400> 62  
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acaaaatggt agccaggtgt tcttgggtcat gccattgaat ttgggtctgt tctcagaaac 180  
tctggaattg aagaagttgc aganaccgaa gataaaatgg tcgtttggag cagaaacacc 240  
tgatttctca tcagtgcata caaccacagg aagacggccc ccaacatt ct tccccagagg 300

45/292

gtttctggggc tgggtgggga tccctcatTT cccatgttaa gcttgaggaa gagatttcag 360  
ggtaggtccc ctgcaggga actactgtc cctcaacttt nggcctcca tagcataatt 420  
tnaaagccag naagggttt ttaaccctt ntttggaag cccgattggc att 474

&lt;210&gt; 63

&lt;211&gt; 457

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(457)

<223> 5' terminal sequence. egf-like module  
containing, mucin-like, hormone receptor-like  
sequence 1 (EMR1) gene.

&lt;400&gt; 63

tctgtcaac ggccaggtac gagaagaata caagaggtgg atcactggga agacgaagcc 60  
cagctcccag tcccagacct caaggatctt gctgtcctcc atgccatccg cttccaagac 120  
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catgnaccag gaacatcggg gttaaccntt tttgttt 457

&lt;210&gt; 64

&lt;211&gt; 3149

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3149)

<223> egf-like module containing, mucin-like,  
hormone receptor-like sequence 1 (EMR1) gene.

&lt;400&gt; 64

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&lt;210&gt; 65

&lt;211&gt; 412

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(412)

<223> 3' terminal sequence. k1aa0427 gene product  
(K1AA0427) gene.

&lt;400&gt; 65

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412

<210> 66  
<211> 442  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(442)  
<223> 5' terminal sequence. k1aa0427 gene product  
(K1AA0427) gene.

<400> 66  
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gggatngagt tagttcattt tt 442

<210> 67  
<211> 5737  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(5737)  
<223> k1aa0427 gene product (K1AA0427) gene.

<400> 67  
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tccgaggcgg cctgcttgcc acagccctgc tcccaaggc ctggtggcct tgccgaagct 4980
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&lt;210&gt; 68

&lt;211&gt; 377

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(377)

<223> 3' terminal sequence. spleen tyrosine kinase  
(SYK) gene.

&lt;400&gt; 68

```

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aaattcacca caggcca 377

```

&lt;210&gt; 69

&lt;211&gt; 323

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(323)

<223> 5' terminal sequence. spleen tyrosine kinase  
(SYK) gene.

&lt;400&gt; 69

```

ttaatttttg aggcgtcca caacttccag gttcccatcc tgcgacttgg tcagcgggtg 60
gaataatctc aagaatcaaa tcatactcct tcccaaagcc tggccacaga aagtcctccc 120
ctgcccaagg gaaccncaa gagagtactg tgtcattcaa tccgtatgag gccaggaact 180
tgcacccggg gcttgacgga caaaggggcc cca gaggagg aagccctacc cntgggacac 240

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agaggtgtta cggaggagcc cntacggcgg gaccccgagg gagnttcagg gcccaagggn 300  
gtttttactt gggggaccga aag 323

&lt;210&gt; 70

&lt;211&gt; 2541

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2541)

&lt;223&gt; spleen tyrosine kinase (SYK) gene.

&lt;400&gt; 70

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caggtgtgtg cccctccggcc cctgaagcat ggccagcagc ggcatggctg acagcgccaa 180  
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cgccctgtcc gtggcccacg ggaggaaggc acaccactac accatcgagc gggagctgaa 360  
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ctttaaaaag aaaaaaaaaa a 2541

<210> 71  
<211> 312  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(312)  
<223> 5' terminal sequence. interleukin 7 receptor  
(IL7R) gene.

<400> 71  
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ctggactgcc agattcatag ggtggatgac attcaagcta gagatgaagt ggaaggtttt 120  
ctgcaagata cgtttctctca gcaactagaa gaatctga ga agcagaggct tngaggggat 180  
gtgcagagcc ccaactgccc atctgaggat gtagtcatca ctccaggaaa gctttgggaa 240  
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tttctccttt t 312

<210> 72  
<211> 1658  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1658)  
<223> interleukin 7 receptor (IL7R) gene.

<400> 72  
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agaactggat gactactcat tctcatgcta tagccagttg gaagtgaatg gatcgagca 180  
ttcactgacc tgtgcttttg aggaccaga tgtcaacacc accaatctg aatttgaaat 240  
atgtggggcc ctctggagg taaagtgcct gaa tttcagg aaactacaag agatatattt 300  
catcgagaca aagaaattct tactgattgg aaagagcaat atatgtgtga aggttggaga 360  
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aattagcaaa accccactac acagtctgca agattctgaa acattgcttt gaccactctt 1560  
cctgagttca gtggcactca acatgagtca agagcatcct gcttctacca tgtggatttg 1620  
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&lt;210&gt; 73

&lt;211&gt; 236

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(236)

<223> 3' terminal sequence. v-myc avian  
myelocytomatosis viral oncogene homolog (MYC)  
gene.

&lt;400&gt; 73

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gggtttatag tacctataat actaggnact atatactagg attgaaa ttc tgtgtaactg 120  
ctataaacgt tttattaaag ttatttacat ttaatgggca atatttacag aggaaacatt 180  
gtgtaaactt taaaattttt taaaanccaa ttcttaaata ccaaactctg taaggg 236

&lt;210&gt; 74

&lt;211&gt; 413

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(413)

<223> 5' terminal sequence. v-myc avian  
myelocytomatosis viral oncogene homolog (MYC)  
gene.

&lt;400&gt; 74

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ctgccaagag ggtcaagttg gacagtgtca gagtccctgag acagatcagc aacaaccgaa 120  
aatgcaccag cccaggttcc tcggacaccg aggagaatgt caagaggcga acacacaacg 180  
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acagcntaca tcctgttccg ttccaaggca ggaggagacc aaaagttcat tttnttgaag 360  
gagggnnttt tttccgggn aacgacgag aaccattttt aaacacaant ttt 413

&lt;210&gt; 75

&lt;211&gt; 2121

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

53/292

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2121)

<223> v-myc avian myelocytomatosis viral oncogene  
homolog (MYC) gene.

&lt;400&gt; 75

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gggcagggt tctcagagg ttggcggga aaaagaacg g agggaggat cgcgctgagt 120
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attgttttta aaaaatttta a 2121
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&lt;210&gt; 76

&lt;211&gt; 260

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(260)

<223> 3' terminal sequence. gata-binding protein 3  
(GATA3) gene.

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&lt;400&gt; 76

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tcacagcact agagaccctg ttaaataggg gatatgagtc agaatggctt attcacagat 60
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aacataattt tgctttctgc cttcaaaaac atatatccat cgcgtttagg cttcatgata 180
ctgctcctgc aaaaatgcaa gtcgaaaggg actgcaggga ctctcgctgg ggggccctgt 240
gagcatcgag cagggtcttt                260

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&lt;210&gt; 77

&lt;211&gt; 409

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(409)

<223> 5' terminal sequence. gata-binding protein 3  
(GATA3) gene.

&lt;400&gt; 77

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tctggtttct tcaattcctt ataagggcac caatcttatt cagagggtc tcaccctcga 120
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ggaggacttc cccaagganc agctnctgtt taaccggggc cgcccttttc caggacacat 360
gttccttccc tggnggccac atnttgnncc ttnaggccan tccagggca 409

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&lt;210&gt; 78

&lt;211&gt; 2365

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2365)

&lt;223&gt; gata-binding protein 3 (GATA3) gene.

&lt;400&gt; 78

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tcccagcctt cccatcccc caccgaaagc aaatcattca acgacccccg accctccgac 60
ggcaggagcc ccccgacctc ccaggcggac cgcccttccc tcccgcgcg ggttccgggc 120
cggcgagag ggcgcgacga cagccgaggc catggagggt acggcggacc agccgcgctg 180
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```

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cattcagttg gcaaaaaaaaa aaaaa 2365
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&lt;210&gt; 79

&lt;211&gt; 328

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(328)

<223> 3' terminal sequence. growth factor  
receptor-bound protein 7 (GRB7) gene.

&lt;400&gt; 79

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ttgtatnttt naaataatct ttattgtcac tagtataaaa cagagcagat caactggcct 60
ctcggctctgt acaaagtgtg gggcgtgaaa ccgctgggct gccccactt ctcccataat 120
tccctgcctt agagcagcag ctccagagct aggagaagga gagggggcca cccaaggcct 180
tcccttgagg agaggggtca ggagtggact ggagtggggg ctgttttcta tctgaggagg 240
gcaaagaagc agaggagaaa actggagtgg cggaacctc ccgntcctca tcccgtcccc 300
tgtggccgat cccanagtcc actnggat 328
```

&lt;210&gt; 80

&lt;211&gt; 428

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(428)



<223> 5' terminal sequence. growth factor  
receptor-bound protein 7 (GRB7) gene.

<400> 80

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caggcctgga ggaagaagac aaaccaccgc ctacgcctgc ccatgccagc ctccggacga 180
gcctcagtgc agccatccac cgcacccaac tctggttcca cgggcgcatt tcccgtgagg 240
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agtcagcggg aacccccagg ggtttttcct ctttttnttg ccaccttgca gaaagtgaag 360
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tgattggc 428
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<210> 81

<211> 2205

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2205)

<223> growth factor receptor-bound protein 7  
(GRB7) gene.

<400> 81

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tgtagagaag cgggagtgga tctgaaataa aatocaggaa tctgggggtt cctagacgga 120
gccagacttc ggaacgggtg tctgtctact cctgtctggg ctctccagg acaaggga c 180
acaactggtt cgttaagcc cctctctcgc tcagacgcca tggagctgga tctgtctcca 240
cctcatctta gcagctctcc ggaagacctt tggccagccc ctgggacccc tctgggact 300
ccccggcccc ctgatacccc tctgcctgag gaggtaaaga ggtcccagcc tctcctcatc 360
ccaaccacgc gcaggaaact tcgagaggag gagagggc gtg ccacctccct cccctctatc 420
cccaaccctt tccctgagct ctgcagtcct ccctcacaga gcccaattct cggggggccc 480
tccagtcaa gggggctgct cccccgcgat gccagccgcc cccatgtagt aaagggttac 540
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tgccaccccc acctagcact ggagcggggt ttggaggacc acgagtccgt ggtggaagtg 720
caggctgcct ggcccggtgg cggagatagc cgcttcgtct tccggaaaaa cttcgccaag 780
tacgaactgt tcaagagctc cccacactcc ctgttcccag aaaaaatggt ctccagc tgt 840
ctcgatgcac aactgggtat atcccatgaa gacctcatcc agaacttcct gaatgctggc 900
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cgctttttct gtttcttgcg ccgatctggc ctctattact ccaccaaggg cacctctaag 1020
gatccgaggg acctgcagta cgtggcagat gtga acgagt ccaacgtgta cgtggtgacg 1080
cagggccgca agctctacgg gatgccact gacttcggtt tctgtgtcaa gcccaacaag 1140
cttcgaaatg gacacaaggg gcttcggatc ttctgcagtg aagatgagca gagccgcacc 1200
tgctggctgg ctgccttcgc cctcttcaag tacgggggtg agctgtacaa gaattaccag 1260
caggcacagt ctgcctatct gcattccatct tgtttgggct cccacacctt gagaagtgcc 1320
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ccccgggagg ctctgagtggt ggccctggag gaggccagg cctggaggaa gaagacaaac 1440
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accaactct ggttccacgg gcgcatttcc cgtgaggaga gccagcggct tattggacag 1560
cagggttggt tagacggcct gttcctggtc cgggagagtc agcggaaacc ccagggtttt 1620
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```

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ccccctctcc ttctcctagc tctggagggt ctgctctagg gcagggaatt atgggagaag 2100  
tgggggcagc ccaggcgggt tcacgcccc cacttt gtac agaccgagag gccagttgat 2160  
ctgctctggt ttatactagt gacaataaag attatttttt gatac 2205

&lt;210&gt; 82

&lt;211&gt; 313

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(313)

<223> 5' terminal sequence. topoisomerase (dna) ii  
beta (180kd) (TOP2B) gene.

&lt;400&gt; 82

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acagacagat aaagttccaa gtaaaacggt agctgctaaa aagggtatgt acttataatt 120  
gattgagtta agcattgg at agagatagtt aatgtaaaag gaaatgtaat ttaatttgaa 180  
actatttgca tttttttatc ataaaacaat taaggaagta taagtgttta taaggaggac 240  
ctctcgtttt ctagccatct gagggcggtta ataaatttct gtaggactta ntttaaagct 300  
gttgantttt taa 313

&lt;210&gt; 83

&lt;211&gt; 4866

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4866)

<223> topoisomerase (dna) ii beta (180kd) (TOP2B)  
gene.

&lt;400&gt; 83

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tcaaagaagt tgtctgttga gagagtgtat cagaagaaga cacaacttga acacattctt 180  
cttcgtcctg atacatatat tgggtcagtg gagccattga cgcagttcat gtgggtgt at 240  
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attccagtag tagaacacaa ggtagagaaa gtttat gttc ctgctttaat ttttgacag 480  
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aaatttaaga tggaaaaact tgacaaggat atttggtccc tcatgactag aagggcata 780  
gatttggtct gttcgtgtag aggggtcaag gtcattgtta atggaaagaa attgcctgta 840  
aatggatttc gcagttatgt agatctttat gtgaaagaca aattggatga aactgg ggtg 900  
gccctgaaag ttattcatga gcttgcaaat gaaagatggg atgtttgtct cacattgagt 960

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 agagatgcaa aagggcgaga ggtcaatgat cttaaaagaa aatctccttc agatctttgg 3540  
 aaagaggatt tagcggcatt tgttgaagaa ctggataaag tggaaatctca agaacgagaa 3600  
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 tcagaatttg gcattccaaa gaagactaca acaccaaagg gtaaaaggccg aggggcaag 4620

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aaaacaacaa gcaagaaacc gaagaagaca tcttttgatc aggattcaga tgtggacatc 4740  
ttcccctcag acttccctac tgagccacct tctctgccac gaaccggctc g gctaggaaa 4800  
gaagtataat attttacaga gtctgatgaa gaagaagatg atgttgattt tgcaatgttt 4860  
aattaa 4866

&lt;210&gt; 84

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(311)

<223> 3' terminal sequence. caspase 4,  
apoptosis-related cysteine protease (CASP4) gene.

&lt;400&gt; 84

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aagttgatta aggagggctg ggctgcttgt ggcttccatt ttcaattgcc aggaaagagg 120  
tagaaatata ttgtcatgga cagtogttct atgggtggca tttagacttt ggcccttgga 180  
gtttcaaatg attgctgtac cttccgaaat acttctctta ggtggcagca ccaagaatat 240  
ttctgggaag catgtgatga gttgtgtgat gaagatagag cccattgtg ctgtctctcc 300  
cagggcacgt t 311

&lt;210&gt; 85

&lt;211&gt; 1291

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1291)

<223> caspase 4, apoptosis-related cysteine  
protease (CASP4) gene.

&lt;400&gt; 85

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gaaaaaagcc acttaaggtg ttggaatccc tgggcaaaga ttctctcact ggtgttttgg 120  
ataacttggt ggaacaaaat gtactgaact ggaaggaaga ggaaaaaag aa atattacg 180  
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agctttgtcc tcatgaagaa ttcttgagac tatgtaaaga aagagctgaa gagatctatc 420  
caataaagga gagaaacaac cgcacagcc tggctctcat catatgcaat acagagttag 480  
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aggacaaacc caagtcacat attgtccagg cctgcagagg tgcaaacctg ggggaactgt 840  
gggtcagaga ctctocagca tccttggaag tggcctcttc acagtcactc gagaacctgg 900  
aggaagatgc tgtttacaag acccacgtgg agaaggactt cattgctttc tgctcttcaa 960

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```
cgccacacaa cgtgtcctgg agagacagca caatgggctc tatottcatc acacaactca 1020
tcacatgctt ccagaaatat tcttggtg ct gccacctaga ggaagtattt cggaaggtag 1080
agcaatcatt tgaaactcca agggccaaag ctcaaagcc caccatagaa cgactgtcca 1140
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cctccttaat caacttcaag gagcaccttc attagtacag ctgcatatt taacattttg 1260
tatttcaata aaagtgaaga caaaaaaaaaa a 1291
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&lt;210&gt; 86

&lt;211&gt; 319

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(319)

&lt;223&gt; 5' terminal sequence. tiss ue inhibitor of metalloproteinase 2 (TIMP2) gene.

&lt;400&gt; 86

```
tggacccatg ggatgagtgt tttattcatg ctgtttccag gaagggatgt cagagctgga 60
ccagtcgaaa cccttgaggg ctttttttgc agttggccac aggggctgtg gaggcctgct 120
tatgggtcct cgatgtcgag aaactcctgc ttgnggaen ccgcg ccgcg tnnccacgca 180
caggagccnt cacttctctt gatgcaggcg aagaacttgg cctggnnccc gttnatgttc 240
ttctctgtga cccagtcctt ccagaggcac tcgtccgggg agganatgta gcacgggatc 300
atngggcanc gcgtgatct 319
```

&lt;210&gt; 87

&lt;211&gt; 1075

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1075)

&lt;223&gt; tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

&lt;400&gt; 87

```
cgagcaaac acatccgtag aaggcagcgc ggccgccga g agccgcagcg ccgctcgccc 60
gccgcccccc acccggccgc ccgcccgggc gaattgcgcc ccgcccctt cccctcgcg 120
ccccgagaca aagaggagag aaagtgttgc cgccgagcgc gggcagggtga ggagggtag 180
ccgcgcggga ggggcccgcg tcggcccgcg ctcagccccc gcccgcgccc ccagcccgc 240
gccgcgagca gcgcccgg ac ccccagcgc cggcccgcgc ccgcccagcc ccccgggccc 300
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tgcttcgccc ggccgacgcc tgcagctgct ccccggtgca cccgcaacag gcgttttgca 420
atgcagatgt agtgatcagg gccaaagcgc tcagtgcgaa ggaagtggac tctggaaacg 480
acatttatgg caaccctatc aagaggatcc agtatgagat caagcagata aagatgttca 540
aagggcctga gaagatatata gagtttatct acacggcccc ctcctcgcca gtgtgtgggg 600
tctcgtgga cgttgaggga aagaaggaat atctcattgc aggaaggcc gagggggacg 660
gcaagatgca catcaccctc tgtgacttca tcgtgccc tg ggacaccctg agcaccaccc 720
agaagaagag cctgaaccac aggtaccaga tgggctgcga gtgcaagatc acgcgctgcc 780
ccatgatccc gtgctacatc tcctccccgc acgagtgcct ctggatggac tgggtcacag 840
agaagaacat caacgggcac caggccaagt tcttcgcctg catcaagaga agtgacggct 900
```

cctgtgctgtg gtaccgcggc gcggcgcccc ccaagcagga gtttctcgac atcgaggacc 960  
cataagcagg cctccaacgc ccctgtggcc aactgcaaaa aaagcctcca agggtttcga 1020  
ctgggtccagc tctgacatcc cttcctggaa acagcatgaa taaaacactc atccc 1075

<210> 88  
<211> 225  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(225)  
<223> 3' terminal sequence. d-dopachrome  
tautomerase (DDT) gene.

<400> 88  
ttttttgaat gaggaagctc ttttcattta ttcanatga ggatgaagaa gaggattatg 60  
tgancacagg aatnttgcac gcgggataat ccaaagctgg ttatctccag gncctcantn 120  
tgccaagaga tctctctgga agaagcagcc agttcacaga tgccctggat ccctccgtgc 180  
ccaatcataa aaaagtcacg accgtcccta tnttgccaat ntgcc 225

<210> 89  
<211> 312  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(312)  
<223> 5' terminal sequence. d-dopachrome  
tautomerase (DDT) gene.

<400> 89  
cgttcctgga gctggacacg aatttgcccg ccaaccgagt gcccgcggn tngagaaac 60  
gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgctg aacgtgacgg 120  
tacggccggg cctggccatg gcgctgagcg ggtccaccga gccctgcgcg cagtgttcca 180  
tctcctocat cggcgtagtg gggcaccgcg agggacaacc gcagccacag cgccatttc 240  
ttttgagttt tttcaccaag gagctaagcc cctgccaggg acccgat ant tattccttt 300  
ttttcccttt gg 312

<210> 90  
<211> 666  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(666)  
<223> d-dopachrome tautomerase (DDT) gene.

&lt;400&gt; 90

```
gatccccggtg ccaggggaccc tgcccagttc caggcgctgc ctaaccaga aacgactggg 60
cgccgcgtcc tggaaaggcc ccagcgcacg gacatctgag gagctgtttc cgttcctctg 120
cccgccatgc cgttcctgga gctggacacg aatttgccc ccaaccgagt gcccgcgggg 180
ctggagaaac gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgcgtg 240
aacgtgacgg tacggccggg cctggcoatg gcgctgagcg ggtccaccga gccctgcgcg 300
cagctgtcca tctcctccat cggcgtagtg ggaccgcgg aggacaaccg cagccacagc 360
gccacttct ttgagtttct caccaaggag ctagccctgg gcc aggaccg gatacttata 420
cgctttttcc ccttgagtc ctggcagatt ggcaagatag ggacggcat gactttttta 480
tgattgggca cggagggatc cagggcattc gtgaactggc tgcttcttcc agagagatct 540
cttggcagag tgagggcctg gagataacca gctttggatt atcccgcatg caacattcct 600
gtgatcacat aatcctcttc ttcctctca tatgaaataa atgaagagag cttcctcatt 660
caaaaa
```

&lt;210&gt; 91

&lt;211&gt; 443

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(443)

&lt;223&gt; 3' terminal sequence. prolactin (PRL) gene.

&lt;400&gt; 91

```
gantttgatg tctctaagga gtcagttttt attttttaag aggagacctg ttacacccaa 60
gcatggattc aaaagagata caactaaaag aagcttgcaa tggaaaggat cattaaggac 120
cttctcagaa atagatgaaa tggatgtggg cttagca gtt gttgttgtgg atgattcggg 180
cacttcaggg agcttgagga taattgtoga ttttatgtga atccctgcgt aggcaatggg 240
agaggttata ataaggcagg aaagggcgag actcttcata agccatctgc aggggatggg 300
aagtccccga ccagacagag gtagatctca tttcttttgg gttttcaggg atgaacctgg 360
gcttgactat ccagcttcca tgnccctctt ggaagccctt ttggttttgc tccctcaatc 420
ttctacagct tttgggttag ggt
```

&lt;210&gt; 92

&lt;211&gt; 243

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(243)

&lt;223&gt; 5' terminal sequence. prolactin (PRL) gene.

&lt;400&gt; 92

```
gaagaatcgg aacatacagg ctttgatata aaaggtttat aaagccaata tctgggaaag 60
agaaaaccgt gagacttcca gatcttctct ggtgaagtgt gtttcctgca acgatcacga 120
acatgaacat caaaggatcg ccatgggaaa gggccctcc tgctgctgct ggggtgttcaa 180
acctgctcct gtgccagagc gtgggcccc ttggcccatc tgtcccgnc gggcttgccc 240
gat
```

<210> 93  
<211> 833  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(833)  
<223> prolactin (PRL) gene.

<400> 93  
aaacatgaac atcaaaggat cgccatggaa agggtcctc ctgtgtctgc tgggtgtcaaa 60  
cctgtctgtg tgccagagcg tggccccctt gcccatctgt cccggcggg ctgcccgatg 12 0  
ccaggtgacc ctgcgagacc tggttgaccg cgccgtctgc ctgtccact acatccataa 180  
cctctctca gaaatgttca gcgaattcga taaacggat acccatggc gggggttcat 240  
taccaaggcc atcaacagct gccacacttc ttcccttgcc acccccgaag acaaggagca 300  
agcccaacag atgaatcaaa aagactttct gagcctgata gtcagcatat tgcgacctg 360  
gaatgagcct ctgtatcatc tggtcacgga agtacgtggt atgcaagaag ccccgaggc 420  
tattctatcc aaagctgtag agattgagga gcaaaccaaa cggcttctag agggcatgga 480  
gctgatagtc agccagggtc atcctgaaac caaagaaaat gagatctacc ctgtctggtc 540  
gggacttcca tccctgcag a tggctgatga agagtctcgc ctttctgctt attataacct 600  
gctccactgc ctacgcaggg attcacataa aatcgacaat tatctcaagc tctgaagtg 660  
ccgaatcatc cacaacaaca actgctaagc ccacatccat ttcattctatt tctgagaagg 720  
tccttaataga tccgttccat tgcaagcttc ttttagttgt atctcttttg aatccatgct 780  
tgggtgtaac aggtctcctc ttaaaaaata aaaactgact cgtagagac atc 833

<210> 94  
<211> 304  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(304)  
<223> 3' terminal sequence. prolactin receptor  
(PRLR) gene.

<400> 94  
actaagcagt gtgcttttat ttcatgaac acatagtttt ataactaaca gcaaaaagta 60  
aatctacaaa tcacagttag gaaacataat gatttgttct ggaatcagct gctggagaaa 120  
gaggcaagtg gttaaaaatg gagcatgaaa ggagctggga gctttagtag tgtcagtcctg 180  
actacattct tgaggcattt cacgtactct gtagtgttac ctgaagaaaa atcacatttt 240  
aaccaatcat tccattagtc aagctatcag tgaaaggagt gtgtaaaaca tgcgggatcc 300  
cggg 304

<210> 95  
<211> 366  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer



<220>  
<221> misc\_feature  
<222> (1)..(366)  
<223> 5' terminal sequence. prolactin receptor  
(PRLR) gene.

<400> 95  
gaggctattg agaagccaga gaatcctgaa acanccacaca cctggaaccc ccantgcata 60  
agcatggaag gcaaaatccc ctatttncat gctggtggat ccaaagtgtc aacatggccc 120  
ttaccacagc ccagccagca caacccaga tcctcttacc acaatattac tgatgtgtgt 180  
gagctggctg tgggccctgc aggtgcaccg gccactctgt tgaatgaagc aggtaaagat 240  
gctttaaaat cctctcaaac cattaagtct agagangag g gnaaggcaac ccaggcagag 300  
ggaggtagga aagcttccat tcttgagnac tgaccagggg tacgncctgg gttgcttgcc 360  
ccaggg 366

<210> 96  
<211> 2723  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2723)  
<223> prolactin receptor (PRLR) gene.

<400> 96  
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ctccctcttt ctggatttta ccgaccgttc gcgaaacagc tttccacaca atggagcttc 120  
atgtcctcgt gcaggaagta ctcatcgact gatgtggcag actttgctcc ctgacaaaac 180  
taaagaactc tcctattcat ggaggcgaac actgaggatg cttccacat gaaccctgaa 240  
gtgaacttct gatacatttc ctgcagcaag agaaggcagc caacatgaag gaaaatgtgg 300  
catctgcaac cgttttcaact ctgctacttt ttctcaac ac ctgccttctg aatggacagt 360  
tacctcctgg aaaacctgag atctttaa atgtgttctcc caataaggaa acattcacct 420  
gctggtggag gcctgggaca gatggaggac ttctaccaa ttattcactg acttaccaca 480  
gggaaggaga gacactcatg catgaatgtc cagactacat aaccgggtggc cccaactcct 540  
gccactttgg caagcagtac acctccatgt ggaggacata catcatgatg gtcaatgcca 600  
ctaaccagat gggaagcagt ttctcggatg aactttatgt ggacgtgact tacatagtgc 660  
agccagaccc tcctttggag ctggctgtgg aagtaaaaca gccagaagac agaaaaccct 720  
acctgtggat taaatggtct ccacctaccc tgattgactt aaaaactggt tggttcac gc 780  
tcctgtatga aattcgatta aaacccgaga aagcagctga gtgggagatc cattttgctg 840  
ggcagcaaac agagttaaag attctcagcc tacatccagg acagaaatac cttgtccagg 900  
ttcgtgcaa accagaccat ggatactgga gtgcatggag tccagcgacc ttcattcaga 960  
tacctagtga cttcaccatg aatgatataa ccgtgt gcat ctctgtggct gtcctttctg 1020  
ctgtcatctg tttgattatt gtctgggcag tggctttgaa gggctatagc atggtgacct 1080  
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tgctagtcga ttcaaaagaa cacccaagtc aaggtatgaa acccacatac ctggatcctg 1320  
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aaccccagc caatccctoc acattctatg atcctgaggc cattgagaag ccagagaatc 1440  
ctgaaacaac ccacacctgg gaccccgagc gcataagcat ggaaggcaaa atcccctatt 1500  
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ccagatcctc ttaccacaat attactgatg tgtgtgagct ggctgtgggc cctgcagggtg 1620  
caccggccac tctgttgaat gaag caggta aagatgcttt aaaatcctct caaaccatta 1680  
agtctagaga agagggaag gcaaccagc agaggagggt agaaagcttc cattctgaga 1740  
ctgaccagga tacgccctgg ctgctgcccc aggagaaaac cccctttggc tccgctaaac 1800  
ccttgagata tgtggagatt cacaaggatg acaaagatgg tgcattatca ttgctaccaa 186 0

65/292

```
aacagagaga gaacagcggc aagcccaaga agcccgaggac tcctgagaac aataaggagt 1920
atgccaaagg gtccgggggtc atggataaca acatcctggg gttgggtgcc gatccacatg 1980
ctaaaaacgt ggcttgcttt gaagaatcag ccaaagaggc cccaccatca ctggaacaga 2040
atcaagctga gaaagccctg gccaaacttca ctgcaaca tc aagcaagtgc aggctccagc 2100
tgggtgggtt ggattacctg gatcccgcat gttttacaca ctcccttcac tgatagcttg 2160
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aatgctcaag aatgtagtca gactgacact actaaagctc ccagctcctt tcatgctcca 2280
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aactgtgatt tgtagattta ctttttgctg ttagttataa aactatgtgt tcaatgaaat 2400
aaaagcacac tgcttagtat tcttgaggga caatgccaat aggtatatcc tctggaaaag 2460
gctttcatga tttggcatgg gacagacgga aatgaaattg tcaaaattgt t taccataga 2520
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aaagaaagaa tgcattccag aacaaattgt ttacataagt tcctatacct tactgacaca 2700
ttgctgatat gcaagtaaga aat                                     2723
```

&lt;210&gt; 97

&lt;211&gt; 365

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(365)

<223> 3' terminal sequence. interleukin 2  
receptor, beta (IL2RB) gene.

&lt;400&gt; 97

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gtacagttac cttttattta tagcgaaaat ggggtttttc atttacagag taacaaagat 60
ttttctttaa ataatgtat ttcaacgaaa atgaactgac ttaaagaaaa aatattaagg 120
aaataatcac aaagatggta cacacggatc attaaaagat acggatgtat aggatacata 180
tgtcacaaat gattaaggac ttaaaaaatg taaccctccc aagaagtggg gagcctccca 240
aagtggggga agggcaaata caatttcnt ttgggggggg ataggngac cccctttgca 300
gagagggggt aggtggggtt tcccccggn acacacaggc aagggtttgg gngccccttg 360
tgggg                                           365
```

&lt;210&gt; 98

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(366)

<223> 5' terminal sequence. interleukin 2  
receptor, beta (IL2RB) gene.

&lt;400&gt; 98

```
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aggggggttg gcaccaagct ctgtccaatc aggtaggctg ggctgaacta gccaatcaga 120
tcaactctgt cttgggcgtt tgaactcagg gagggaggcc cttgggagca ggtgcttggt 180
gacaaggctc cacaagcgtt gagccttgga aaggtagaca agcgttg agc cactaagcag 240
aggaccttgg gtcccaata caaaaatacc tactgctgag aggggntgct gaccattttg 300
```

gtcaaggatt tcngtttgcc ttatatccca aataaantcc cttttttttn aggttttntt 360  
agtntt 366

<210> 99

<211> 4034

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(4034)

<223> interleukin 2 receptor, beta (IL2RB) gene.

<400> 99

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ggagagcgcg cgctgccacc gcccatgtc tcagccaggg ctcccttctt cggtccacc 120  
ctgtggatgt aatggcgggc cctgctctgt cctggcgtct gccctctctc atcctcctcc 180  
tgccctggc tactcttgg gcatctgcag cggtgaatgg cacttcccag ttcacatgct 240  
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tcccgtgag tcaagcatcc tgggcctgca acctgaccc cggagcccca gattctcaga 420  
aactgaccac agttgacatc gtcaccctga ggggtgctgt ccgtgagggg gtgcgatgga 480  
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ccctcaagt tgtccacgtg gagaccaca gatgaacat aagctgggaa atctcccaag 600  
cctccacta ctttgaaga cacctggagt tcgaggcccg gacgctgtcc ccaggccaca 660  
cctgggagga ggccccctg ctgactctca agcagaagca ggaatggatc tgcctg gaga 720  
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ctgggttttc tgccccagcc tctccttcc ctccccctcc cgtccacagg gcagcctgag 2220  
cgtgctttcc aaaaacccaa tatggccacg ctccccctcg gttcaaaacc ttgcacagg 2280  
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acttccctga ctcttcaagt gccggtttg ctctcctgg agggaagcac tgcctccctt 2520  
aatctgccag aaacttctag cgtcagtgct ggaggagaa gctgtcaggg acccaggcg 2580

67/292

```

cctggagaaa gaggccctgt tactattcct ttgggatctc tgaggcctca gagtgccttg 2640
ctgctgtatc tttaatgctg gggcc caagt aagggcacag atccccccac aaagtggatg 2700
cctgctgcat cttccacacag tggcttcaca gaccacaag agaagctgat ggggagtaaa 2760
ccctggagtc cgaggcccag gcagcagccc cgctagtgg tgggccctga tgctgccagg 2820
cctgggacct cccactgccc cctccactgg aggggtctcc tctgcagctc agggactggc 2880
acactggcct ccagaagggc agctccacag ggcagggcct cattattttt cactgcccc 2940
gacacagtgc ccaacacccc gtcgtatacc ctggatgaac gaattaatta cctggcacca 3000
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aaaataagta caat
4034

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&lt;210&gt; 100

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(444)

<223> 3' terminal sequence. gata-binding protein 3  
(GATA3) gene.

&lt;400&gt; 100

```

tttctatttt tttattttct tttaatgcat caaacaactg tggccagtga aaggaaacaa 60
aactggcagt ttgtccattt gaatatcaga cctagtttct tcttaatttc cacacta ttt 120
ctcccatatt ccttaaaactt cttggcatcc ttcattgcctt acagctaccc agatgcaata 180
aagtcattgt acagtatttc ttacaatata agttatatgg caatgttcag gcattttttt 240
ttttcacagg cactaggagg accctgttta aatgggggat atgaggtcag gaatgggctt 300
attcacagga tgggggggtcc cggattcagg tgggt tgggg ancacaggac accacagggtg 360
aggctccctt tgccaaaggt ggggccaaac ataatttttg cttttctggc ccttcaaaaa 420
catatttccn tcgcgttttg gggg
444

```

&lt;210&gt; 101

&lt;211&gt; 396

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

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<221> misc\_feature  
<222> (1)..(396)  
<223> 5' terminal sequence. gata-binding protein 3  
(GATA3) gene.

<400> 101  
gcaatgggga cctgtctgc aatgcctgtg gntctactac aagcttcaca atattaacag 60  
acccttgact atgaagaagg aagcatcc a gaccagaaac cgaaaaatgt ctagcaaadc 120  
caaaaagtgc aaaaagtgc tgactcactg gaggacttcc ccaagaacag ctggtttaac 180  
ccggccgccc tctccagaca catgtcctcc ctgagccaca tctcgccctt cagccactcc 240  
agccacatgc tgaccacggc ccacgccgat ggcacccgcc atccagcctg tcctttggga 300  
ccacaccacc cctccagctg ggtcaccgcc ntgggtttag agccttgtnn gatggttcac 360  
agggggcccc cagcgagagt tncctgnagt tccttt 396

<210> 102  
<211> 416  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(416)  
<223> 5' terminal sequence. placental growth  
factor, vascular endothelial growth factor -related  
protein (PGF) gene.

<400> 102  
attcggcact aggggagacc caagggcagg gggaagagga ggagagagaa gcagagaccc 60  
acagactgcc acctgtgcgg cgatgctgtt ccccgagta acccaccct tggaggagag 120  
agaccccgca cccggctcgt gtatttatta ccgtcacact cttcagtgc tctgtctggt 180  
acctgcctc tatttattag ccaactgtt ccctgtgaa tgcctcgtc ccttcaagac 240  
gaggggcagg gaaggacagg accctcagga attcagtgc ttcaacaacg tga gagaaag 300  
agagaagcca gccacagacc cctggggagc ttccgcttt tgaaagaagc aagacaagt 360  
ggccttgtt aggggcaagg ttagggccca ggaggccctn gggaagtttt tcaggg 416

<210> 103  
<211> 1645  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1645)  
<223> placental growth factor, vascular  
endothelial growth factor -related protein (PGF)  
gene.

<400> 103  
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tccccgggac ccgctgccc ctgcgcgcc cgcccgccg ggccgctccc cgtcgggttc 120  
cccagccaca gccttaccta cgggctcctg actccgcaag gcttcagaa gatgctcgaa 180  
ccaccggccg gggcctcggg gcagcagtga gggaggcgtc cagccccca ctcagctctt 240  
ctctcctgt gccaggggct ccccggggga tgagcatggt ggttttcctt cggagcccc 300

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tggctcggga cgtctgagaa gatgccggtc atgaggctgt tcccttgctt cctgcagctc 360
ctggccgggc tggcgtgcc tgcgtgccc cccagcagt gggccttgct tgctgggaac 420
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&lt;210&gt; 104

&lt;211&gt; 309

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(309)

<223> 5' terminal sequence. ubiquitin protein  
ligase e3a (human papilloma virus e6 -associated  
protein, angelman syndrome) (UBE3A) gene.

&lt;400&gt; 104

```

ttcggcanag gggaaatgaa gcctgcacga atgagttttg tgcttcctgt ccaacttttc 60
ttcgtatgga taataatgca gc agctatta aagccctcga gctttataag antagggcaa 120
aactctgtga tcctcatccc tccaagaaag gagcaagctc agcttacctt gagaactcga 180
aaggtgcccc caacaactcc tgctctgaga taaaaatgaa caaggaaagg gcgctaggaa 240
ttggatttta aagatgtgac ttactttaac aggaaggagg aagggtatta tggaaaattt 300
tctttggac 309

```

&lt;210&gt; 105

&lt;211&gt; 2628

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2628)

&lt;223&gt; ubiquitin protein ligase e3a (human

papilloma virus e6 -associated protein, angelman syndrome) (UBE3A) gene.

<400> 105

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cttcgtatgg ataataatgc agcagctatt aaagccctcg agctttataa gattaatgca 240
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aaaggtgccc ccaacaactc ctgctctgag ataaaaatga aca agaaagg cgctagaatt 360
gatttttaag atgtgactta cttaacagaa gagaagggtat atgaaattct tgaattatgt 420
agagaaagag aggattatcc ccttttaatc cgtgttattg gaagagtttt ttctagtgtc 480
gaggcattgg tacagagctt ccggaaggtt aaacaacaca ccaaggaaga actgaaatct 540
cttcaagcaa aagatgaaga c aagatgaa gatgaaaagg aaaaagctgc atgttctgct 600
gctgctatgg aagaagactc agaagcatct tctcaagga taggtgatag ctacacagga 660
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catacttgct ttaatgtgct tttacttccg gaatactcaa gcaaagaaaa acttaaagag 2580
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<210> 106

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc\_feature

<222> (1)..(363)

<223> 3' terminal sequence. oncogene tc21 (TC21)  
gene.

<400> 106

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aattttaatt ctagcacctg aagctataca agggatgct ctataaactt catgggactg 60
tcgtacacac ttgataaagt gacaactgtg caataccact tagcatctca aaatcag gaa 120
catactattg aattgcttaa acacaatcca caganttaaa aacaaaatca ggatgccatc 180
cacagttata ctaattatcc attaaaaggc ttacacttaa tacttgaant aacaatcaat 240
atctagncgg ggnatactgg aaagtggatt tcagnggtct catcctgttg gtactctatt 300
ggggnggggt ttcttgagggt aggttatggg ggact gggnc caaggntggg ggggtaccacc 360
cag 363
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<210> 107

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(408)

<223> 5' terminal sequence. oncogene tc21 (TC21)  
gene.

<400> 107

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ctgatggcca aaataccaaa tgctgttgtt atttatggat taaaaactgc ttataaaacc 120
ctgtgttact actcctaactc ttggagatga taatatct ta tgtgggtcaaa tatttggact 180
catttaggac ttagataattt cagtgtactt gattttttta tttaactctt ttccacagcc 240
acgctaaggg taaaaaggaa taatttcctt ctgtcttcct tttcaagtat ttctgggtaa 300
gggattcaaa aaactaaaaac tgtttttggt tgtaatatata aatatgggat tgatctttcc 360
ggggtcagag atgattaatg tttttgctat atacttttat acatgnnt 408
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<210> 108

<211> 612

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(612)

<223> oncogene tc21 (TC21) gene.

<400> 108

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gggggcgcgg tgggcaagtc ggcgctcacc atccagttca tccagtccta ttttgtaacg 120
gattatgatc caaccattga agattcttac acaagcaggt gtgtgataga tgacagagca 180
gcccggttag atattttgga tacagcagga caagaagagt t tggagccat gagagaacag 240
tatatgagga ctggcgaagg cttcctgttg gtcttttcag tcacagatag aggcagtttt 300
gaagaaatct ataagtttca aagacagatt ctcagagtaa aggatcgtga tgagttccca 360
atgattttta ttggaataaa agcagatctg gatcatcaaa gacaggtaac acaggaagaa 420
ggacaacagt tagcacggca gcttaaggta acatacatgg aggcacagc aaagattagg 480
atgaatgtag atcaagcttt ccatgaactt gtccgggtta tcaggaaatt tcaagagcag 540
gaatgtcctc cttcaccaga accaacacgg aaagaaaaag acaagaaagg ctgccattgt 600
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gtcattttct ag

6 12

<210> 109  
<211> 592  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(592)  
<223> 5' terminal sequence. tyrosine kinase with  
immunoglobulin and epidermal growth facto r  
homology domains (TIE) gene.

<400> 109  
ngtcggagag aacctagcct ccaagattgc agacttcggc ctttctcggg gagaggaggt 60  
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ctacagtgtc tataccacca agagtgatgt ctggtccttt ggagtccttc tttgggagat 1 80  
agtgagcctt ggaggtacac cctactgtgg catgacctgt gccgagctct atgaaaagct 240  
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gcgttcagtg ctggcgggac cgtccctatg agcgaccccc ctttgcccag attgcgctaa 360  
cagctaggcc gcatgctggg aagccaggga aggcctatgt gaacatgttc gctgtttgag 420  
aacttcaatt aacgcgggca ttgatgccac agctgaggag gnetgagctg ccattccagcc 480  
agaactnggt ctggtggccg gagcaaattt ggtgtctaaa ctgtgaccag ttnaacctta 540  
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<210> 110  
<211> 3845  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3845)  
<223> tyrosine kinase with immunoglobulin and  
epidermal growth factor homology domains (TIE)  
gene.

<400> 110  
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gactggcatg aagcccagga tgggcgggtc ctgctgcagc tcccaaattg gcagccacca 600  
tcgagcggca tctacagtgc cacttacctg gaagccagcc ccttgggcag cg ccttcttt 660  
cggctcatcg tgcggggttg tgggctggg cgcctggggc caggctgtac caaggagtgc 720  
ccaggttgcc tacatggagg tgtctgccac gaccatgacg gcgaatgtgt atgccccct 780  
ggcttcactg gcaccccgctg tgaacaggcc tgcagagagg gccgttttgg gcagagctgc 840

73/292

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caggagcagt gccaggcat atcaggctgc cggggcctca ccttctgcct cccagacccc 900
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&lt;210&gt; 111

&lt;211&gt; 202

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(202)  
<223> 3' terminal sequence. autocrine motility  
factor receptor (AMFR) gene.

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acccatgggg canantnatg ag 202

<210> 112  
<211> 450  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(450)  
<223> 5' terminal sequence. autocrine motility  
factor receptor (AMFR) gene.

<400> 112  
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cccagtgagg tggaagactt cgaggctcgt gggagcgtt tctccaagtc tgctgatgag 240  
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cgccgcggga aacggaggct ttcagaagca 450

<210> 113  
<211> 1810  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1810)  
<223> autocrine motility factor receptor (AMFR)  
gene.

<400> 113  
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gcccagtgag gtggaagact tcgaggctcg tgggagcgc tctccaagt ctgctgatga 180  
gagacagcgc atgctggctg cagcgtaagg acgaactcct ccagcaagct cgcaaactgt 240  
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&lt;210&gt; 114

&lt;211&gt; 248

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(248)

<223> 3' terminal sequence. homo sapiens mrna;  
 cdna dkfzp434c136 (from clone dkfzp434c136) (EST  
 R81127) gene.

&lt;400&gt; 114

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gaaattccaa aatcactcta gttattcac ataatatagn atttgattcc attcttttgn 60
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cangaaatac ttgatctaaa ctgggagggt ccaacacaat tttttttttt aatgggnctt 240
gccacctt 248

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&lt;210&gt; 115

&lt;211&gt; 415

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(415)

<223> 3' terminal sequence. b-cell cll/lymphoma 2  
 (BCL2) gene.

<400> 115  
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tgtcacttct tttgttactt ctttatagtt cccaccatt gatTTTTttt ttaatgcccc 240  
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caaataaanc caaactacag tgacaggata atgtttttaca ggtaattccn tgggccgggg 360  
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<210> 116  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(468)  
<223> 5' terminal sequence. b-cell cll/lymphoma 2  
(BCL2) gene.

<400> 116  
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aagcttgatg ggagctcaga atttccactg ttcaagaaa agncagtaga ggggtgtngc 420  
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<210> 117  
<211> 6030  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(6030)  
<223> b-cell cll/lymphoma 2 (BCL2) gene.

<400> 117  
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&lt;210&gt; 118

&lt;211&gt; 343

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(343)

<223> 5' terminal sequence. v-erb-b2 avian  
erythroblastic leukemia viral oncogene homolog 2  
(neuro/glioblastoma derived oncogene homolog)  
(ERBB2) gene.

&lt;400&gt; 118

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&lt;210&gt; 119

&lt;211&gt; 4530

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4530)

<223> v-erb-b2 avian erythroblastic leukemia viral  
oncogene homolog 2 (neuro/glioblastoma derived  
oncogene homolog) (ERBB2) gene.

&lt;400&gt; 119

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```

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ttgtccattt gcaaatatat tttgaaaa c 4530

```

<210> 120  
 <211> 319  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(319)  
 <223> 5' terminal sequence. mouse double minute 2,  
 human homolog of; p53-binding protein (MDM2) gene.

```

<400> 120
naattatttc ccctagttga cctgtctata agagaattat atatttctaa ctatataacc 60
ctaggaattt agacaacctg aaatttattc acatatatca aagtgagaaa atgcctcaat 120
tcacatagat ttctttctct tagtataatt gacctacttt ggtagtggga a tagtgaata 180
cttactataa tttgacttga atatgtaggc tcacccctta caccaactcc taattttaaa 240
taatttctac tctgtcttaa atgaggaggc acttgggnnt ttttttttct taaatatggg 300
atatggacat ttaaatggt 319

```

<210> 121  
 <211> 2372  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature

<222> (1)..(2372)

<223> mouse double minute 2, human homolog of;  
p53-binding protein (MDM2) gene.

<400> 121

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gcaagaagcc gagcccgagg ggcggccgcg acccctctga ccgagatcct gctgctttcg 120
cagccaggag caccgtccct ccccgatta gtgcgtacga gcgccagtg ccctggcccg 180
gagagtggaa tgatccccga gggccagggc gtcgtgcttc cgcagtagtc agtccccgtg 240
aaggaaactg gggagtcttg agggaccccc gactccaagc gcgaaaaccc cggatggtga 300
ggagcaggca aatgtgcaat accaacaatgt ctgtacctac tgatggtgct gtaaccacct 360
cacagattcc agcttcggaa caagagaccc tggtttagacc aaagccattg cttttgaagt 420
tattaaagtc tgttggtgca caaaaagaca cttatactat gaaaga gggt cttttttatc 480
ttggccagta tattatgact aaacgattat atgatgagaa gcaacaacat attgtatatt 540
gttcaaatga tcttctagga gatttggttg gcgtgccaaag cttctctgtg aaagagcaca 600
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aagagaatta tatatttcta actatataac cctaggaatt tagacaacct gaaatttatt 1860
cacatatata aaagtgagaa aatgcctcaa ttoacataga tttcttctct ttagtataat 1920
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caaagtgtcg ggattacagg catgagccac cg 2372
```

<210> 122

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(343)

<223> 3' terminal sequence. gata-binding protein 3  
(GATA3) gene.

&lt;400&gt; 122

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atgcttataa tattattcca acagactgta tta aaggcag tgatcactaa cacagancac 60
gacagggcga ngaggcagcc nggcccataa ncaggacgtg gccnntcggc caggggttcgc 120
tgacatgcac gctggttagct catacactgc taccctcagc acaggctgca ggaataggga 180
caagacagat gccgcgggac tcttaggaag ctatttaata aatatcatcc aaanacaaaa 240
tgggaaaagg aaacaaggaa accctccggg gcacaaccac cttaggggcc aactggaatg 300
gtaattctag gttttatttc caacccaaaa nttgaggaga gga 343
```

&lt;210&gt; 123

&lt;211&gt; 258

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(258)

<223> 3' terminal sequence. src homology 3  
domain-containing protein hip-55 (HIP-55) gene.

&lt;400&gt; 123

```
cgagtgaant atgttgaggg aacatgttgt gtctgccgtt tttgaatacc cagggtgagg 60
gcttgcccat ctgcatcccc acttcccata gcccaggcag agggac agag aaatggagtn 120
gggagcacag agcaggctcc aacaagacaa attccctgct gccaaaccac catgatccac 180
tctgactttg gncacaaact ctgctaaaaa caattctcta cgttcactgt tcccaagggg 240
canttttaaa cagtgggtg 258
```

&lt;210&gt; 124

&lt;211&gt; 443

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(443)

<223> 5' terminal sequence. src homology 3  
domain-containing protein hip-55 (HIP-55) gene.

&lt;400&gt; 124

```
gccagggtc agtgggcaag ggctctgtgc cgtngnccctg tacgactacc atgcagccga 60
cgacacagag atctcctttg accccgagaa cctcatcacg ggcacgcagg tgatcgacga 120
aggctgggtg cgtggctatg ggccggatca tntgttingca tgttccctgc caactacgtg 180
gagctcattg agtgaggctg agggcacatc ttgcccttcc cctctcagac atggcttc ct 240
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ccccagttga ggattgagge ntcagggttc cctccggnnt gggcagattc agccttttca 360
cccaaattg cagcaattgg cntgggtgat ttcccacaaa tcnttcctgg cattcccccg 420
acctttccca gacagtttg ttt 443
```

&lt;210&gt; 125

&lt;211&gt; 1331

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1331)

<223> src homology 3 domain-containing protein  
hip-55 (HIP-55) gene.

&lt;400&gt; 125

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accgagaagt ccccgaccga ctgggtctctc ttacctatg aaggcaacag caatgacatc 120
cgcggtggctg gcacagggga ggggtggcctg gaggagatgg tggaggagct caacagcggg 180
aaggtgatgt acgccttctg cagagtgaag gaccccaact ctggactgcc caaatattgtc 240
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ttccctgcc aactacgtgga gtcattgag tgag gctgag ggcggccgct agactagtct 1320
agagaaaaaa c 1331
```

&lt;210&gt; 126

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(430)

<223> 3' terminal sequence. cathepsin d (lysosomal  
aspartyl protease) (CTSD) gene.

&lt;400&gt; 126

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gtatttccat gtcagctggg gctctcagcc gcccaagggg aggacaacag aggtcagctg 60
cagaggaagg ctggcaccag ccccaatccc aacccacact ccaggccaat acatgcccct 120
gggactggct cagtccagc accaccctgc aggtccaac aaggtgggtt ttgtcccctc 180
tactccttc cagtcattcc tcaggcctct agcggcctca tcctcaacgg gcccgggaca 240
ctgaacagg aggtgggca gagccagctg ggncccaagc tnggcaagag gggccctcag 300
gcagggcagg ttttncaagg gagggncccc gaggacggcc ttgggtnttg g ggttaagggc 360
ttaanccagt cngggctttg gtaaggggcc ggnaagggat tcntgggna aattaaagg 420
aanccccagg 430
```

&lt;210&gt; 127

<211> 339  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(339)  
 <223> 5' terminal sequence. cathepsin d (lysosomal  
 aspartyl protease) (CTSD) gene.

<400> 127  
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 acatgatccc ctgtgagaag gtgtccacc c tggccgcgat cacactgaag ctgggaggca 120  
 aaggctacaa gctgtcccca gaggactaca cgctcaaggt gtgcgaggcc gggaagaccc 180  
 tctgcctgag cggttcatg ggcattgaca tcccgcacc cagcggnac tctggatcct 240  
 ggggcgacgt cttcattcgg ccgttantac attgtgtttt gaccgtgaca acaacagggt 300  
 tgggtttcgc gaggcttgcc cgcttttagt ttcccaagg 339

<210> 128  
 <211> 1988  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(1988)  
 <223> cathepsin d (lysosomal aspartyl protease)  
 (CTSD) gene.

<400> 128  
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 ggggctctgt ggaggacctg attgccaaag gcccgcgttc aaagtactcc caggcggtgc 180  
 cagccgtgac cgaggggccc attcccagag tgctcaagaa ctacatggac gccagttact 240  
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 gggaggccac caagcagcca ggcacacct tcatcgagc caagttcgat ggcacccctg 600  
 gcatggccta ccccgcatc tccgtcaaca acgtgctgcc cgtcttcgac aacctgatgc 660  
 agcagaagct ggtggaccag aacatcttct ccttctacct gagcagggac ccagatgcgc 720  
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 ccagcgggct gacctgtgc aaggagggt gtgaggccat tgtggacaca ggcacttccc 900  
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 acacacaccc acacactcgc ccgcccactg tcctgggcgc cctggaagcc ggccggccaa 1380  
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```

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1988

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<210> 129

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(385)

<223> 5' terminal sequence. insulin-like growth factor 1 receptor (IGF1R) gene.

<400> 129

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<210> 130

<211> 4989

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(4989)

<223> insulin-like growth factor 1 receptor (IGF1R) gene.

<400> 130

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87/292

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&lt;210&gt; 131

&lt;211&gt; 470

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(470)

<223> 5' terminal sequence. insulin receptor  
(INSR) gene.

&lt;400&gt; 131

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&lt;210&gt; 132

&lt;211&gt; 4691

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4691)

&lt;223&gt; insulin receptor (INSR) gene.

&lt;400&gt; 132

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aaaaaaccaa a 4691
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<210> 133  
<211> 451  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(451)  
<223> 5' terminal sequence. forkhead box ola  
(rhabdomyosarcoma) (FOXO1A) gene.

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<210> 134  
<211> 5723  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(5723)  
<223> forkhead box ola (rhabdomyosarcoma) (FOXO1A)  
gene.

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91/292

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<210> 135  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(466)  
 <223> 3' terminal sequence. epidermal growth  
 factor receptor (avian erythroblasti c leukemia  
 viral (v-erb-b) oncogene homolog) (EGFR) gene.

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<210> 136  
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 <212> DNA  
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<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(450)

<223> 5' terminal sequence. epidermal growth  
factor receptor (avian erythroblastic leukemia  
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 136

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<210> 137

<211> 5532

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(5532)

<223> epidermal growth factor receptor (avian  
erythroblastic leukemia viral (v-erb-b) oncogene  
homolog) (EGFR) gene.

<400> 137

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&lt;210&gt; 138

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(378)

<223> 3' terminal sequence. tek tyrosine kinase,  
endothelial (venous malformations, multiple  
cutaneous and mucosal) (TEK) gene.

&lt;400&gt; 138

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&lt;210&gt; 139

&lt;211&gt; 447

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(447)

<223> 5' terminal sequence. tek tyrosine kinase,  
endothelial (venous malformations, multiple  
cutaneous and mucosal) (TEK) gene.

&lt;400&gt; 139

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&lt;210&gt; 140

&lt;211&gt; 4138

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4138)

<223> tek tyrosine kinase, endothelial (venous  
malformations, multiple cutaneous and mucosal)  
(TEK) gene.

&lt;400&gt; 140

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&lt;210&gt; 141

&lt;211&gt; 395

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(395)

<223> 3' terminal sequence. tumor necrosis factor  
receptor superfamily, member 6 (TNFRSF6) gene.

&lt;400&gt; 141

```
taattccaaa cacaaggggc aaaaaaatcc tccataaatg gaagttcttt aggtggttcc 60
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atttcttaaa attcacattt aatacaaaact ttcaaagata tttaaacgta ggatagtagt 180
aaggagaatc ttaaattctta gaaacttggg ggtatgacaa gagcaattcc taaatccaga 240
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gattggcaaa cctgggggttc angacatggt cacaac 395
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&lt;210&gt; 142

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(461)

&lt;223&gt; 5' terminal sequence. tumor necrosis factor

receptor superfamily, member 6 (TNFRSF6) gene.

<400> 142

```
t c g t a a t t g g   c a t c a a c t t c   a t g g a a a g a a   a g a a g c g t a t   g a c a c a t t g a   t t a a a g a t c t   60
c a a a a a a g c c   a a t c t t t t g t a   c t c t t g c a g   a   g a a a a t t c a g   a c t a t c a t c c   t c a a g g a c a t   120
t a c t a g t g a c   t c a g a a a a t t   c a a a c t t c a g   a a a t g a a a t c   c a a a g c t t g g   t c t a g a g t g a   180
a a a a c a a c a a   a t t c a g t t c t   g a g t a t a t g c   a a t t a g t g t t   t g a a a g a t t   c t t a a t a g c t   240
g g c t g t a a a t   a c t g c t t g g t   t t t t t a c t g g   g t a c a t t t t a   t c a t t t a t t a   g c g c t g a a g a   300
g c c a a c a t a t   t t g t a g g t t t   t t a a t a t c t c   c a t g g a t t c t   g c c t c c a a g g   g t g t t t a a a a   360
t c t a g t t g g g   g g a a c a a a c   t t c c t t c a a g   g g t t a a a t g c   n g t g g c c t g g   c t a a g t a c c c   420
c c a t t a g g g a   g t g t t t g c c g   g g g g t t g n a a   g g t t t a g g t t   t                               461
```

<210> 143

<211> 2551

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2551)

<223> tumor necrosis factor receptor superfamily,  
member 6 (TNFRSF6) gene.

<400> 143

```
g c a a g a g t g a   c a c a c a g g t g   t t c a a a g a c g   c t t c t g g g g a   g t g a g g g a a   g   c g g t t t a c g a   60
g t g a c t t g g c   t g g a g c c t c a   g g g g c g g g c a   c t g g c a c g g a   a c a c a c c c t g   a g g c c a g c c c   120
t g g c t g c c c a   g g c g g a g c t g   c c t c t t c t c c   c g c g g g t t g g   t g g a c c c g c t   c a g t a c g g a g   180
t t g g g g a a g c   t c t t t c a c t t   c g g a g g a t t g   c t c a a c a a c c   a t g c t g g g c a   t c t g g a c c c t   240
c c t a c c t c t g   g t t c t t a c g t   c t g t t g c t   a g   a t t a t c g t c c   a a a a g t g t t a   a t g c c c a a g t   300
g a c t g a c a t c   a a c t c c a a g g   g a t t g g a a t t   g a g g a a g a c t   g t t a c t a c a g   t t g a g a c t c a   360
g a a c t t g g a a   g g c c t g c a t c   a t g a t g g c c a   a t t c t g c c a t   a a g c c c t g t c   c t c c a g g t g a   420
a a g g a a a g c t   a g g g a c t g c a   c a g t c a a t g g   g g a t g a a c c a   g a c t g c g t g c   c c t g c c a a g a   480
a g g g a a g g a g   t a c a c a g a c a   a a g c c c a t t t   t t c t t c c a a a   t g c a g a a g a t   g t a g a t t g t g   540
t g a t g a a g g a   c a t g g c t t a g   a a g t g g a a a t   a a a c t g c a c c   c g g a c c c a g a   a t a c c a a g t g   600
c a g a t g t a a a   c c a a a c t t t t   t t t g t a a c t c   t a c t g t a t g t   g a a c a c t g t g   a c c c t t g c a c   660
c a a a t g t g a a   c a t g g a a t c a   t c a a g g a a t g   c a c a c t c a c c   a g c a a c a c   c a   a g t g c a a a g a   720
g g a a g g a t c c   a g a t c t a a c t   t g g g t g g c t   t g t g t c t t t   c t t t t g c c a a   t t c c a c t a a t   780
t g t t t g g g t g   a a g a g a a a g g   a a g t a c a g a a   a a c a t g c a g a   a a g c a c a g a a   a g g a a a a c c a   840
a g g t t c t c a t   g a a t c t c c a a   c c t t a a a t c c   t g a a a c a g t g   g c a a t a a a t t   t a t c t g a t g t   900
t g a c t t g a g t   a a a t a t a t c a   c c a c t a   t t g c   t g g a g t c a t g   a c a c t a a g t c   a a g t t a a a g g   960
c t t t g t t c g a   a a g a a t g g t g   t c a a t g a a g c   c a a a a t a g a t   g a g a t c a a g a   a t g a c a a t g t   1020
c c a a g a c a c a   g c a g a a c a g a   a a g t t c a a c t   g c t t c g t a a t   t g g c a t c a a c   t t c a t g g a a a   1080
g a a a g a a g c g   t a t g a c a c a t   t g a t t a a a g a   t c t c a a a a a a   g c c a a t c t t t   g t a c t c t t g c   1140
a g a g a a a a t t   c a g a c t a t c a   t c c t c a a g g a   c a t t a c t a g t   g a c t c a g a a a   a t t c a a a c t t   1200
c a g a a a t g a a   a t c c a a a g c t   t g g t c t a g a g   t g a a a a a c a a   c a a a t t c a g t   t c t g a g t a t a   1260
t g c a a t t a g t   g t t t g a a a a g   a t t c t t a a t a   g c t g g c t g t a   a a t a c t g c t t   g g t t t t t t a c   1320
t g g g t a c a t t   t t a t c a t t t a   t t a g c g c t g a   a g a g c c a a c a   t a t t t g t a g a   t t t t t a a t a t   1380
c t c a t g a t t c   t g c c t c c a a g   g a t g t t t a a a   a t c t a g t t g g   g a a a a c a a a c   t t c a t c a a g a   1440
g t a a a t g c a g   t g g c a t g c t a   a g t a c c c a a a   t a g g a g t g t a   t g c a g a g g a t   g a a a g a t t a a   1500
g a t t a t g c t c   t g g c a t c t a a   c a t a t g a t t c   t g t a g t a t g a   a t g t a a t c a g   t g t a t g t t a g   1560
t a c a a a t g t c   t a t c c a c a g g   c t a a c c c c a c   t c t a t g a a t c   a a t a g a a g a a   g c t a t g a c c t   1620
t t t g c t g a a a   t t c a g t t t a c   t g a a c a g g c a   g g c c a c t t t g   c c t c t a a a t t   a c c t c t g a t a   1680
a t t c t a g a g a   t t t t a c c a t a   t t t c t a a a c t   t t g t t t a t a a   c t c t g a g a a g   a t c a t a t t t a   1740
t g t a a a g t a t   a t g t a t t t g a   g t g c a g a a t t   t a a a t a a g g c   t c t a c c t c a a   a g a c   c t t t g c   1800
a c a g t t t a t t   g g t g t c a t a t   t a t a c a a t a t   t t c a a t t g t g   a a t t c a c a t a   g a a a a c a t t a   1860
a a t t a t a a t g   t t t g a c t a t t   a t a t a t g t g t   a t g c a t t t t a   c t g g c t c a a a   a c t a c c t a c t   1920
t c t t t c t c a g   g c a t c a a a a g   c a t t t t g a g c   a g g a g a g t a t   t a c t a g a g c t   t t g c c a c c t c   1980
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tccatttttg ccttggtgct catottaat g gcctaata gca ccccaaaaca tggaaatata 2040
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taaaatatag gtaaaagtac gtaattaaat a 2551

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&lt;210&gt; 144

&lt;211&gt; 434

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(434)

<223> 3' terminal sequence. cyclin-dependent  
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

&lt;400&gt; 144

```

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gccacgtgg catgccctgt ccatagcctc tactgccacc atcttaaaat gtctgactcc 360
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gttcgntgga cggt 434

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&lt;210&gt; 145

&lt;211&gt; 257

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(257)

<223> 5' terminal sequence. cyclin-dependent  
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

&lt;400&gt; 145

```

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ttctccaaga ggaagcccta atccgcccac aggaagcctg cagtcctgga agcgcgaggg 180
cctcaaaggc cntnctnaca tcttctgcct tagtctcagt ttgtgtgtct taattattat 2 40
ttgtgtttta aattttt 257

```

&lt;210&gt; 146

&lt;211&gt; 2121

99/292

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2121)

<223> cyclin-dependent kinase inhibitor 1a (p21,  
cip1) (CDKN1A) gene.

&lt;400&gt; 146

```
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cgaccttctc catcaccccc atccctcccc agttcattgc actttgatta gcagcggaac 1740
aaggagtcag acattttaag atggtggcag tagaggctat ggacagggca tgccacgtgg 1800
gctcatatgg ggctgggagt agttgtcttt cctggcacta acgttgagcc cctggaggca 1860
ctgaagtgtc tagtgtactt ggagtattgg ggtctgacct caaacacc tt ccagctcctg 1920
taacatactg gcctggactg tttctctctg gctccccatg tgcctgggt cccgtttctc 1980
cacctagact gtaaacctct cgagggcagg gaccacaccc tgtactgttc tgtgtcttcc 2040
acagctctcc ccacaatgct gaataacag cagggtgtca ataatgatt cttagtgtgact 2100
ttaaaaaaaaa aaaaaaaaaa a                                     2121
```

&lt;210&gt; 147

&lt;211&gt; 452

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

<222> (1)..(452)

<223> 3' terminal sequence. phospholipase a2,  
group iia (platelets, synovial fluid) (PLA2G2A)  
gene.

<400> 147

```
gatttgctaa ttgctttatt cagaagagac cccccggagt acagcttctt tggttaagca 60
cggagttgag gtggaggaga gcagtagaag gctggaaatc tgctggatgt ctcattctgg 120
gtgggtatag aagggtcctt gcctggcctc taggatgggt gagggatgct ttctgcatgg 180
ccaaggaact tggtaggggt agggagggag ggtatgagag agggaaattc agcactgggt 240
ggaaggtttc cagggaagag gggactcagc aacgaggggt gctccctctg cagtntttat 300
tggaatagta ctggtacttt ttattgtagg tcgtcttntt tctagcaaaa cagggtngca 360
gcagccttat cacacttca c acagttgact tctgcaggag tccnttttt gcacaggttg 420
attctgctcc ccgaagttac taaacttttt tt 452
```

<210> 148

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(379)

<223> 5' terminal sequence. phospholipase a2,  
group iia (platelets, synovial fluid) (PLA2G2A)  
gene.

<400> 148

```
tggagtcctc tgagagagcc accaaggagg agcaggggag cgacggccgg ggcagaagtt 60
gagaccaccc agcagaggag ctaggccagt ccatctgc at ttgtcaccca agaactctta 120
ccatgaagac cctcctactg ttggcagtga tcatgatctt tggectactg caggcccatg 180
ggaatttgggt gaatttccac agaatgatca agttgacgac aggaaaggaa gccgcactca 240
gttatggctt ctacggctgc cactgtggcg tgggttgagc aggatcccc aaggatgcaa 300
cggattcgct gctgtgtcac tcatgactgt ttgtacaaa cgtctgggag aaacgtgggt 360
tnttggcacc aaatttttt 379
```

<210> 149

<211> 854

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(854)

<223> phospholipase a2, group iia (platelets,  
synovial fluid) (PLA2G2A) gene.

<400> 149

```
gaattcccaa ctctggagtc ctctgagaga gccaccaagg aggagcaggg gagcgacggc 60
cggggcagaa gttgagacca ccagcagag gagctaggcc agtccatctg catttgtc ac 120
ccaagaactc ttacatgaa gaccctccta ctgttggcag tgatcatgat ctttggccta 180
ctgcaggccc atgggaattt ggtgaatttc cacagaatga tcaagttgac gacaggaaag 240
gaagccgcac tcagttatgg cttctacggc tgccactgtg gcgtgggtgg cagaggatcc 300
```

```

ccaaggatg caacggatcg ctgctgtgtc actcat gact gttgctacaa acgtctggag 360
aaacgtggat gtggcaccaa atttctgagc tacaagtta gcaactcggg gagcagaatc 420
acctgtgcaa aacaggactc ctgcagaagt caactgtgtg agtgtgataa ggctgctgcc 480
acctgttttg ctagaacaaa gacgacctac aataaaaagt accagtacta ttccaataaa 540
cactgcagag ggag cacccc tcgttgtgtg gtccctctt ccctggaaac cttccaccca 600
gtgctgaatt tccctctctc ataccctccc tccctaccct aaccaagttc cttggccatg 660
cagaaagcat ccctcaccca tcctagaggc caggcaggag cccttctata cccaccaga 720
atgagacatc cagcagattt ccagccttct actgctctcc tccacctcaa ctccgt gctt 780
aaccaaagaa gctgtactcc ggggggtctc ttctgaataa agcaattagc aaatcaaaaa 840
aaaaaaagga attc 854

```

<210> 150

<211> 224

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc\_feature

<222> (1)..(224)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)  
gene.

<400> 150

```

ggttgagcac aggnacttt attgatgna catgacaagg tgcggtccc taggcccctc 60
ccctnttcaa ggggtctaca tggcaact nt gaggagggga gattcagtgt ggtgggggac 120
tgagtntggc agggactccc cagcagttag ggtctctctc ttcctcttnt gctcttntctg 180
ggngtgggtg nccagggntn ttactccttg gaggccatnt gggc 224

```

<210> 151

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc\_feature

<222> (1)..(359)

<223> 5' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)  
gene.

<400> 151

```

gcgctgagta cgtcgtggag tccactggcg tcttcaccac catggagaag gctgggggctc 60
atttgcaggg gggagccaaa agggatcatc tcttgcccc ctctgctgat gcccccatgt 120
tctcatggg tgtgaaccat gagaagtatg acaacagcct caagatcatc agcaatgcct 180
cctgcaccac caactgctta gcaccctgg gccaaaggta tccatgacaa ctttggtatc 240
gtggaaggac tcatgaccac agtccatgcc atcactgcca c ccagaagac tgtggatggc 300
ccctncggga aactgtgggc gtgatggccg cgggggttctt tcagaacatc atccctgcc 359

```

<210> 152

<211> 1283

<212> DNA/RNA

102/292

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1283)

<223> glyceraldehyde -3-phosphate dehydrogenase  
(GAPD) gene.

&lt;400&gt; 152

```
ctctctgctc ctctgttcg acagtcagcc gcatcttctt ttgcgtcgcc agccgagcca 60
catcgctcag acaccatggg gaaggtgaag gtcggagtca acggatttgg tcgtattggg 120
cgctgggtca ccagggtctg ttttaactct ggta aagtgg atattgttgc catcaatgac 180
cccttcattg acctcaacta catggtttac atgttccaat atgattccac ccatggcaaa 240
ttccatggca ccgtcaaggc tgagaacggg aagcttgtca tcaatggaaa tcccatcacc 300
atcttccagg agcgagatcc ctccaaaatc aagtggggcg atgctggcgc tgagtacgtc 360
gtggagtcca ctggcgtctt caccaccatg gagaaggctg gggctcattt gcagggggga 420
gccaaaaggg tcatcatctc tgcccccctc gctgatgccc coatgttcgt catgggtgtg 480
aaccatgaga agtatgacaa cagcctcaag atcatcagca atgcctcctg caccaccaac 540
tgcttagcac ccctggccaa ggtcatccat gacaactttg gtatcgtgga agga ctcattg 600
accacagtcc atgccatcac tgccaccag aagactgtgg atggcccctc cgggaaactg 660
tggcgtgatg gccgcggggc tctccagaac atcatecctg cctctactgg cgctgccaag 720
gctgtgggca aggtcatccc tgagctgaac gggaagctca ctggcatggc cttccgtgtc 780
cccactgcca acgtgtcagt ggtggacctg ac ctgccgtc tagaaaaacc tgccaaatat 840
gatgacatca agaaggtggt gaagcaggcg tcggagggcc ccctcaaggg catcctgggc 900
tacactgagc accaggtggt ctccctctgac ttcaacagcg acaccactc ctccacctt 960
gacgtctggg ctggcattgc cctcaacgac cactttgtca agctcattc ctggtatgac 1020
aacgaatttg gctacagcaa cagggtgggt gacctcatgg ccacatggc ctccaaggag 1080
taagaccctt ggaccaccag cccagcaag agcacaagag gaagagagag accctcactg 1140
ctggggagtc cctgccacac tcagtcccc accacactga atctcccctc ctcacagttg 1200
ccatgtagac cccttgaaga ggggaggggc ctaggagacc gcacctgt c atgtaccatc 1260
aataaagtac cctgtgctca acc 1283
```

&lt;210&gt; 153

&lt;211&gt; 361

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(361)

<223> 3' terminal sequence. jun b proto -oncogene  
(JUNB) gene.

&lt;400&gt; 153

```
tacttaata gattcaatan aaagaacaaa cacacacaaa cacaacacg tcttaaaata 60
aactctttag agactaagtg cgtgttctt ttccacagta cgggtgcagag aggggagggc 120
agggggcggg ggtcccttcc caatgtcccc gggggttga gta ccaggcg gcggggccag 180
ctccntant ncgccccctc ttccctccc tgtaaatac acaaataat tatattcaat 240
ntgaatcng tctntttcca gcagaaaaaa aacatacaaa aaaaagtggg aagggggggg 300
cttntttaa cgttcggang ttggaaggnc ttggggcnc aggggtaggg angggccgag 360
t 361
```

&lt;210&gt; 154

<211> 401  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(401)  
<223> 5' terminal sequence. jun b proto -oncogene  
(JUNB) gene.

<400> 154  
agcgcacaa agtngagcgc angccttgcg gaaccggctn gcggccacca agtgccggaa 60  
gcggaantgg gagcgcacgc ggcttgggag gacaaggtga agacgctcaa ggccgagaac 120  
gcgggntgt cgagtaccgc cggcttcctc cgggagcagg tggcccagct caaacagaag 180  
gtcatgaccc acgtnagc aa cggctntnag ctgctgcttn ggtcaaggg acacgccttc 240  
tggaacgttc cctgcccctt tacgggacac ccccttcgtt tnggacggtt nggcacacgg 300  
tttcccaactn ggggtccagg gtagcaggcg gtgggnnacc cacctggggg acntaggggg 360  
cgnccgcaaa ccacattngg attccggcc ttcttaacct t 401

<210> 155  
<211> 1797  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1797)  
<223> jun b proto-oncogene (JUNB) gene.

<400> 155  
ccagcaggga gctgggagct gggggaaacg acgc caggaa agctatcgcg ccagagaggg 60  
cgacgggggc tcgggaagcc tgacagggtc ttgcgacaca gctgccggct ggctgctacc 120  
cgcccgcgcc agcccccgag aacgcgcgac caggcaccca gtccggtcac cgcagcggag 180  
agctcgccgc tcgtgcagc gagggccgga gcggcccgcc agggaccctc ccagaccgc 240  
ctgggcccgc cggatgtgca ctaaaatgga acagcccttc taccacgacg actcatacac 300  
agctacggga tacggccggg cccctggtgg cctctctcta cagactaca aactcctgaa 360  
accgagcctg gcgtcaacc tggccgaccc ctaccggagt ctcaaagcgc ctggggctcg 420  
cggacccgcc ccagagggcg gcggtggcgg cagctacttt tctggtcagg gctcg gacac 480  
cggcgcgtct ctcaagctcg cctcttcgga gctggaacgc ctgattgtcc ccaacagcaa 540  
cggcgtgata acgacgacgc ctacaccccc gggacagtag ttttaccccc gcgggggtgg 600  
cagcggtgga ggtgcagggg gcgcaggggg cggcgctacc gaggagcagg agggcttcgc 660  
cgacggcttt gtcaaagccc tggacgatct gca caagatg aaccacgtga cccccccaa 720  
cgtgtccctg ggcgctaccg gggggccccc ggctggggcc gggggcgtct acgccggccc 780  
ggagccacct cccgtttaca ccaacctcag cagctactcc ccagcctctg cgtcctcggg 840  
aggcgcgggg gctgccgtcg ggaccgggag ctcgtaccgc acgaccacca tcagctacct 900  
cccaacgcgc ccgcccttcg ccggtggcca cccggcgcag ctgggcttgg gccgcggcgc 960  
ctccaccttc aaggaggaac cgcagaccgt gccggaggcg cgcagcggg acgccacgcc 1020  
gccggtgtcc cccatcaaca tgaagacca agagcgcac aaagtggagc gcaagcggct 1080  
gcggaaccgg ctggcgcca ccaagtgcg gaagcgggag ctggagcgca t cgcgcgcct 1140  
ggaggacaag gtgaagacgc tcaaggccga gaacgcgggg ctgtcgagta ccgccggcct 1200  
cctccgggag caggtggccc agctcaaaca gaaggtcatg acccagctca gcaacggctg 1260  
tcagctgctg cttgggggtca agggacacgc cttctgaacg tcccctgcc ctttacggac 1320  
accccctcgc ttggacggct gggcac acgc ctcccactgg ggtccagggg gcaggcgggtg 1380  
ggacccacc ctgggacctt ggggcgcgc aaaccacact ggactccggc cccctaccc 1440



104/292

tgcgcccagt ccttccacct cgacgtttac aagccccccc ttccactttt tttgtatgt 1500  
tttttttctg ctggaaacag actcgattca tattgaatat aatataattg tgtatttaac 1560  
agggagggga agagggggcg atcgggcg agctggcccc gccgcctggt actcaagccc 1620  
gcggggacat tgggaagggg acccccgcct cctgcctcc cctctctgca ccgtactgtg 1680  
gaaaagaaac acgcacttag tctctaaaga gtttatitta agacgtgttt gtgtttgtgt 1740  
gtgtttgttc tttttattga atctatttaa gtaaaaaaaaa aattggttct ttattaa 1797

&lt;210&gt; 156

&lt;211&gt; 335

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(335)

<223> 3' terminal sequence. cellular retinoic  
acid-binding protein 2 (CRABP2) gene.

&lt;400&gt; 156

aagcatttta ataaaattaa caaataaata ttctaaactg tataggctac agggacaaag 60  
ggtagaagct agagggccag tctttcctgc tcaggccctc aagtcctctt tagagagacc 120  
ctgctctggg ctggtttggg gctaggactg ctgacttggg gaggcgggga gtgaaccggg 180  
aatgggtgat ctgggctctt gcagccattc ctctttgttg gtgtagggga ggagagaaga 240  
ggtcaaagaa agcaagaccc tgcaagaggc atcccagtga cccccagaag tgactggggt 300  
aaggggagcg ctatcctagg anggtggggg tgggt 335

&lt;210&gt; 157

&lt;211&gt; 481

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(481)

<223> 5' terminal sequence. cellular retinoic  
acid-binding protein 2 (CRABP2) gene.

&lt;400&gt; 157

gcctggactt gtcttgggtt ccagaacctg acgaccggc gacgcgacgt ctct tttagac 60  
taaaagacag tgtccagtgc tccagcctag gagtctacgg ggaccgcctc ccgcgccgcc 120  
accatgccca acttctctgg caactggaaa atcatccgat cggaaaactt cgaggaattg 180  
ctcaaagtgc tnggggtgaa tgtgatgctg aggaagattg ctgtggctnc agcgtccaag 240  
ccagcagtng agatcaaaca ggaggagac act ttctaca tcaaaacctc caccaccgtg 300  
cggcaccaca gagattaact tcaagggtng ggaggagttt gagggagcag antgtgggtg 360  
gggaggccct gttaaggagc ngggtgaaat ggggagagtg aggattaaat ggtcttttga 420  
gcagaagttc ctgaagggng aggggccccca agaentcttg gacngagaa tttccccacg 480  
t 481

&lt;210&gt; 158

&lt;211&gt; 969

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(969)

<223> cellular retinoic acid-binding protein 2  
(CRABP2) gene.

&lt;400&gt; 158

```
agctttgggg ttgtccctgg acttgtcttg gttccagaac ctgacgaccc ggcgacggcg 60
acgtctcttt tgactaaaag acagtgtcca gtgctccagc ctaggagtct acgggggaccg 120
cctcccgcgc cgccaccatg cccaacttct ctggcaactg gaaaatcatc cgatcggaaa 180
acttcgagga attgctcaaa gtgctggggg tgaatgtgat gctgaggaag attgctgtgg 240
ctgcagcgtc caagccagca gtggagatca aacaggaggg agacactttc tacatcaaaa 300
cctccaccac cgtgcgcacc acagagatta acttcaaggt tggggaggag tttgaggagc 360
agactgtgga tgggaggccc tgtaagagcc tggtgaaatg ggagag tgag aataaaatgg 420
tctgtgagca gaagctoctg aagggagagg gcccgaagac ctggtggacc agagaactga 480
ccaacgatgg ggaactgac ctgaccatga cggcggatga cgttgtgtgc accagggtct 540
acgtccgaga gtgagtggcc acaggtagaa ccgcggccga agcccaccac tggccatgct 600
caccgcctcg cttcactgcc cct ccgtcc caccocctcc ttctaggata gcgctcccct 660
taccocagtc acttctgggg gtacttgga tgctcttgcc aggtcttgcc tttctttgac 720
ctctctcttc ctccctaca ccaacaaaga ggaatggctg caagagccca gatcacccat 780
tcggggttca ctcccgcct cccaagtca gcagtcctag ccccaaacca gccagagca 840
gggtctctct aaaggggact tgagggcctg agcaggaaaag actggccctc tagcttctac 900
cctttgtccc tgtagcctat acagtttaga atatttattt gttaatttta ttaaaatgct 960
ttaaaaaaa
```

&lt;210&gt; 159

&lt;211&gt; 344

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(344)

<223> 3' terminal sequence. activin a receptor  
type ii-like 1 (ACVRL1) gene.

&lt;400&gt; 159

```
cgcgntgga ggggaggtgg ccccgntcc gccgangaan tgcgcccg cc acccgagag 60
cncacagagg gaccattgac cttgggctcc ccaggaag gccttctgat gctgctgatg 120
gccttggtga ccaggggaga cctgtgaag ccgtctcggg gccgctggg gacctgcacg 180
tgtgagagcc cacattgcaa ggggcctacc tgccgggggg cctgggtgca cagtagtgct 240
tgggtgcggg aggaggggag gcacccc cag ggaacattcg gggntgcggg aantttgcac 300
agggaagtct tgcagggggg gcgccccacc gatttcgttc aacc 344
```

&lt;210&gt; 160

&lt;211&gt; 416

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(416)  
<223> 5' terminal sequence. activin a receptor  
type ii-like 1 (ACVRL1) gene.

<400> 160  
gtcagtctcc cggaaccagg actgttcac cctcgaggag aagatcttga cggccacact 60  
ctcaccgtgc cacaagcccc gccacacttc gccatagcgc cttttccccc acactccacc 120  
aaggcaacct gccgtngcca ctgtcctctg caccagggaa ggggagccct gagccactcc 180  
ctgtgggtgg cagtcaactgt ccagggaggt cccccaacat gctgttcgcc ctgcttcaga 240  
tgcttttcag ggatgaggat gggattttcc cagcttcgct gttgcagggc cacgttgctt 300  
tttccttgcc tncgttcggg acatggccac agggcccagg ggacaaccag g gggccacca 360  
gggggnccag gcaanggcca agncacgggg ggcccagggt ttnaaggggc cagttt 416

<210> 161  
<211> 1970  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1970)  
<223> activin a receptor type ii-like 1 (ACVRL1)  
gene.

<400> 161  
aggaaacggt ttattaggag ggagtgggtg agctgggcca ggcaggaaga cgctggaata 60  
agaaacattt ttgtccagc ccccatccca gtcccgggag gctgccgcgc cagctgcgcc 120  
gagcgagccc ctcccgggt ccagcccgtt cgggggccgc gccggacc c agcccgggt 180  
ccagcgctgg cggtgcaact gcggccgcgc ggtggagggg aggtggcccc ggtccgcga 240  
aggtagcgc cccgccacce gcagagcggg cccagaggga ccatgacctt gggctcccc 300  
aggaaaggcc ttctgatgct gctgatggcc ttggtgacct agggagacct tgtgaagccg 360  
tctcggggcc cgctggtgac ctgcacg tgt gagagcccac attgcaaggg gcctacctgc 420  
cggggggcct ggtgcacagt agtctggtg cgggaggagg ggaggcacc ccaggaacat 480  
cggggctgct ggaacttgca caggagctc tgcagggggc gccccaccga gttcgtcaac 540  
cactactgct gcgacagcca cctctgcaac cacaacgtgt cctggtgct ggaggccacc 600  
caacctcctt cggagcagcc gggaacagat ggccagctgg ccctgacctt gggccccgtg 660  
ctggccttgc tggccctggt ggccctgggt gtccctgggc tgtggcatgt ccgacggagg 720  
caggagaagc agcgtggcct gcacagcgag ctgggagagt ccagtctcat cctgaaagca 780  
tctgagcagg gcgacacgat gttgggggac ctctggaca gtgactg cac cacagggagt 840  
ggctcagggc tccccttctt ggtgcagagg acagtggcac ggcaggttgc cttggtggag 900  
tgtgtgggaa aaggccgcta tggcgaagtg tggcggggct tgtggcacgg tgagagtgtg 960  
gccgtcaaga tcttctctc gagggatgaa cagtcctggt tccgggagac tgagatctat 1020  
aacacagtat tgctcagaca cgac aacatc ctaggcttca tgcctcaga catgacctcc 1080  
cgaaactcga gcacgcagct gtggctcatc acgcactacc acgagcacgg ctccctctac 1140  
gactttctgc agagacagac gctggagccc catctggctc tgaggctagc tgtgtccgcg 1200  
gcatgcggcc tggcgcacct gcacgtggag atcttcggtt cacagggcaa accagccatt 126 0  
gcccaccgcg acttcaagag ccgcaatgtg ctggtcaaga gcaacctgca gtgttgcata 1320  
gccgacctgg gcttgctgt gatgactca caggcgagc attacctgga catcggaac 1380  
aaccgagag tgggcaccaa gcggtacatg gcacccgagg tgctggacga gcagatccgc 1440  
acggactgct ttgagtcta caagtggact gacatctg gg cctttggcct ggtgctgtgg 1500  
gagattgccc gccggaccat cgtgaatggc atcgtggagg actatagacc acccttctat 1560  
gatgtggtgc ccaatgacct cagctttgag gacatgaaga aggtggtgtg tgtggatcag 1620  
cagaccccca ccatccctaa ccggttggt gcagacccgg tcctctcagg cctagctcag 1680  
atgatgcggg agtgctggt cccaaacccc tctgcccagc tcaccgcgct gcggatcaag 1740  
aagacactac aaaaaattag caacagtcca gagaagccta aagtgattca atagcccagg 1800

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agcacctgat tcctttctgc ctgcaggggg ctgggggggt ggggggcagt ggatggtgcc 1860  
ctatctgggt agaggtagtg tgagtgtggt gtgtgctggg gatgggcagc t gcgcctgcc 1920  
tgctcggccc ccagcccacc cagccaaaaa tacagctggg ctgaaacctg 1970

&lt;210&gt; 162

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(407)

<223> 5' terminal sequence. lim domain protein  
(RIL) gene.

&lt;400&gt; 162

gtgacctgc gcgggccttc gccctggggc ttccgcctgg tngggccgng gacttcagcg 60  
cgccctcac catctocagg gtccatgctg gcagcaaggc tcatntggct gccctgtgcc 120  
caggagacct gatccaggcc atcaatggtg agagcacaga gctcatgac a cacctggang 180  
cacagaaccg catcaagggc tgccacgac acctcacact gtctgtgagc aggcctgagg 240  
gcaggagctg gcccagtgcc cctgatgaca gcaaggctca ggcacacagg atccacatcg 300  
ntcctgagat ccaggacggc agcccaacaa ccagcaggcg gccctcaggc accgggactt 360  
gggccagaag atnggcagan caagnct ggg gtttttncat atggaca 407

&lt;210&gt; 163

&lt;211&gt; 1130

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1130)

&lt;223&gt; lim domain protein (RIL) gene.

&lt;400&gt; 163

tgagagtcog gctcaggctc cggctgoggc tccagcccgc gatgcccacat tccgtgaccc 60  
tgcgcgggcc ttccgcctgg ggcttcogcc tgggtgggccc ggacttcagc gcgcccctca 120  
ccatctcacg ggtccatgct ggcagcaagg cctcattggc tgccctgtgc ccaggagacc 180  
tgatccaggc catcaatggt gagagcacag agctcatgac acacctg gag gcacagaacc 240  
gcatcaaggg ctgccacgat cacctocacac tgtctgtgag caggcctgag ggcaggagct 300  
ggcccagtgcc ccctgatgac agcaaggctc aggcacacag gatccacatc gatcctgaga 360  
tccaggacgg cagcccaaca accagcaggc ggccctcagg caccgggact gggccagaag 420  
atggcagacc aagcctggga tctcc atatg gaaaaccccc ttgctttcca gtccctcaca 480  
atggcagcag cgaggccacc ctgccagccc agatgagcac cctgcatgtg tctccacccc 540  
ccagcgctga ccagcagag gectcccgcg gagccgggag cagagtcgac ctgggctccg 600  
aggtgtacag gatgtgcgg gagccggccg agcccgtggc cgcggagccc aagcagtcag 660  
gctccttcog ctacttgca ggcattgctag aggcggcgca gggcggggat tggcccgggc 720  
ctggcgggccc ccggaacctc aagcccacgg ccagcaagct gggcgctccg ctgagcggcc 780  
tgcaggggct gcccgagtg acgcgtgct gccacggaat cgtgggcacc atcgtcaagg 840  
aacgggacaa gctctaccat ccagagtgct tcatgtgcag tgact gcggc ctgaacctca 900  
agcagcgtgg ttacttcttt ctggacgagc ggctctactg tgagagccac gccaaaggcg 960  
gcgtgaagcc gcccgagggc tacgacgtgg tggcggtgta ccccaatgcc aaggtggaac 1020  
tcgtctgagc tgggacctg ctcccacccc tgcttcttaa ggtccctgct cggccggtgt 1080

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aaatatgttt caccctgtcc c tctaataaa gtcctctgc tcaaaaaaaaa

1130

&lt;210&gt; 164

&lt;211&gt; 310

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(310)

&lt;223&gt; 5' terminal sequence. shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

&lt;400&gt; 164

anattcggaa cgagggatcc ctcttatgtc aacgtccaga acctagacaa ggcccggcaa 60  
gcagtgggtg gtgctgggcc cccaatcct gctatcaatg gcagtgcacc ccgggacctg 120  
tttgacatga agcccttcga agatgctctt cgcggtgc cto cacctcccca gtcgggtgtcc 180  
atgncatgag agctccgagg ggagccctgg gttccatggg aagctgagcc ggccgggaggc 240  
tgaggcactg ctggcagctt caatggggat ttcnnggtac gggagagcac gaccacacng 300  
gggcaatatg 310

&lt;210&gt; 165

&lt;211&gt; 3664

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3664)

&lt;223&gt; shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

&lt;400&gt; 165

atggggcctg aaactgtctg ggtctgagct ggggagcgga agccacttgt ccctctccct 60  
ccccaggact tctgtgactc ctgggccaca gaggtccaac cagggttaagg gcctggggat 120  
accccctgcc tggccccctt gccaaaactg gcaggggggc caggctgggc agcagcccct 180  
ctttcacctc aactatggat ctctgcccc ccaagcccaa gtacaatcca ct ccggaatg 240  
agtctctgtc atcgctggag gaaggggctt ctgggtccac cccccggag gagctgcctt 300  
ccccatcagc ttcatecctg gggcccatcc tgctcctct gcctggggac gatagtccca 360  
ctacctgtg ctctctcttc ccccgatga gcaacctgag gctggccaac ccggtgggg 420  
ggcgcccagg gtctaagggg gagccaggaa gggcagctga tgatggggag gggatcgatg 480  
gggcagccat gccagagtca ggccccctac ccctcctcca ggacatgaac aagctgagtg 540  
gaggcggcgg gcgcaggact cgggtggaag ggggccagct tgggggcgag gagtggacct 600  
gccacgggag ctttgtcaat aagcccacgc ggggctggct gcatcccaac gacaaagtca 660  
tgggaccggg gggttcctac ttggttcggt acatgggttg tgtggaggtc ctccagtcaa 720  
tgctgtccct ggaattcaac accgggactc aggtcaccag ggaggccatc agtctggtgt 780  
gtgaggctgt gccgggtgct aagggggcga caaggaggag aaagccctgt agccgcccgc 840  
tcagctctat cctggggagg agtaacctga aatttgctgg aatgccaatc actctcaccg 900  
tctccaccag cagcctcaac ctcatggccg cagactgcaa acagatcatc gcccaaccacc 960  
acatgcaatc tatctcattt gcatccggcg gggatccgga cacagccgag tatgtgcct 1020  
atgttgccaa agaccctgtg aatcagagag cctgccacat tctggagtgt cccgaagggc 1080  
ttgcccagga tgcatcagc accattg gcc aggccttcga gttgcgcttc aaacaatacc 1140

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tcaggaaccc acccaaactg gtcaccctc atgacaggat ggctggcttt gatggctcag 1200
catgggatga ggaggaggaa gagccacctg accatcagta ctataatgac ttcccgggga 1260
aggaaccccc cttggggggg gtggtagaca tgaggcttcg ggaaggagcc gctccagggg 1320
ctgctcgacc cactgcaccc aatgccaga ccccagcca cttgggagct acattgcctg 1380
taggacagcc tgttggggga gatocagaag tccgaaaca gatgccacct ccaccacct 1440
gtccaggcag agagcttttt gatgatccct cctatgtcaa cgtccagaac ctagacaagg 1500
cccggcaagc agtgggtggt gctgggcccc ccaatcctgc tatcaatggc agtgaccccc 1560
gggacctgtt tgacatgaag cccttcgaag atgctcttcg ggtgcctcca cctccccagt 1620
cgggtgtccat ggctgagcag ctccgagggg agccttggtt ccatgggaag ctgagccggc 1680
gggaggctga ggcaactgctg cagctcaatg gggacttctt ggtacgggag agcacacca 1740
cacctggcca gtatg tgctc actggcttgc agagtgggca gcctaagcat ttgctactgg 1800
tggacctga ggggtgtggt cggactaagg atcaccgctt tgaaagtgtc agtcacctta 1860
tcagctacca catggacaat cacttgcccc tcatctctgc gggcagcgaa ctgtgtctac 1920
agcaacctgt ggagcggaaa ctgtgatctg ccctagcgct ctcttcaga agat gccctc 1980
caatcctttc caccctattc cctaactctc gggacctcgt ttgggagtgt tctgtgggt 2040
tggccttgtg tcagagctgg gactagcatg cactctgggt ttcatatcca gctgagtga 2100
agggtttgag tcaaaagcct gggtgagaat cctgcctctc cccaaacatt aatcacaaa 2160
gtattaatgt acagagtggc ccctcacct g ggctttcct gtgccaacct gatgccctt 2220
cccaagaag gtgagtgtt gtcattgaaa atgtcctgtg gtgacaggcc cagtgaaca 2280
gtcacccttc tgggcaagg ggaacaaatc acacctctgg gcttcagggt atcccagacc 2340
cctctcaaca cccgcccccc ccatgtttta actttgtgcc ttgaccatc tcttaggtct 2400
aatgatattt tatgaaaca gttcttgac ccctgaatc ttcaatgaca gggatgcaa 2460
caccttcttg gcttctggga cctgtgttct tgctgagcac cctctccggt ttgggttggg 2520
ataacagagg caggagtggc agctgtcccc tctccctggg gatatgcaac ccttagagat 2580
tgccccagag cccactccc ggccaggcgg gagatggacc cc tcccttgc tcagtgcctc 2640
ctggccgggg cccctcacc caaggggtct gtatatacat ttcataaggc ctgccctccc 2700
atgttgcatg cctatgtact ctgcgcaaaa gtgcagccct tccctctgaa gcctctgcc 2760
tgccctccct tctgggaggg cggggtgggg gtgactgaat ttgggcctct tgtacagtta 2820
actctcccag gtgatt ttg tggaggtgag aaaaggggca ttgagactat aaagcagtag 2880
acaatcccc caatacatct gttaggttg aactgcattc ttttaaagt ttatatgcat 2940
atattttagg gctgctagac ttactttcct attttcttt ccattgctta ttcttgagca 3000
caaatgata atcaattatt acatttatac atcacccttt tgacttttcc aagccc tttt 3060
acagctcttg gcattttcct cgcctaggcc tgtgaggtaa ctgggatcgc accttttata 3120
ccagagacct gaggcagatg aaatttattt ccatctagga ctagaaaaac ttgggtctct 3180
taccgcgaga ctgagaggca gaagtcagcc cgaatgcctg tcagtttcat ggaggggaaa 3240
cgcaaaacct gcagttcctg agtaccttct acaggcccg cccagcctag gcccggggtg 3300
gccacaccac agcaagcgg ccccccctct tttggccttg tggataagg agagttgacc 3360
gttttcatcc tggcctcctt ttgctgtttg gatgtttcca cgggtctcac ttataccaaa 3420
gggaaaactc ttcattaaag tccgtatttc ttctaaaaaa aaaaaaaaaa aaatacattt 3480
atacatcacc tttttgactt ttccaagccc ttttacagct cttggcattt tcttcgcta 3540
ggcctgtgag gtaactggga tcgcaccttt tataccagag acctgaggca gatgaaattt 3600
atttccatct aggactagaa aaacttgggt ctcttaccgc gagactgaga ggcagaagtc 3660
agcc 3664

```

&lt;210&gt; 166

&lt;211&gt; 449

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(449)

&lt;223&gt; 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase ( GAPD)  
gene.

&lt;400&gt; 166

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```
gagcacaggg tnttttattg atggtacatg acaaggtgcg gctccctagg cccctcccct 60
cttcaagggg tctacatgga aactgtgagg aggggagatt cagtgtggtg ggggactgag 120
tntggcaggg actccccagc agtgagggtc tctctcttcc tcttgtgctc ttgctggggc 180
tggtggtcca ggggtcttac tccttgaggg ccatgtgggc atgaggtcca ccacctgtt 240
gctgtagcca aattcgttgt cataccaggg aaatgagctt gacaaagtgg tcgttgaggg 300
caatgccagc cccagcnttc gaaggtggag gantgggttt cgctnttgaa gtcagaggag 360
accacctggg tgctcagttt agcccaggga tgcccttgag ggggccctcc gacgttt ttt 420
tcaccacctt tttgatntca tcatntttt 449
```

&lt;210&gt; 167

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(467)

&lt;223&gt; 5' terminal sequence.

glyceraldehyde -3-phosphate dehydrogenase (GAPD)  
gene.

&lt;400&gt; 167

```
tggtcgacag tcagccgcat cttcttttgc gtcgccagcc gagccacatc gctgagacac 60
catggggaag gtgaaggctg gagtcaacgg atttggtcgt attgggcgcc tggtcaccag 120
ggctgctttt aactctggta aagtggata t tggtgccatc aatgaccctt tcattgacct 180
caactacatg gtttacatgt tccaatatga ttccacccat gggcaaattc catgggcacc 240
gtcaaggctg agaacgggaa gcttgtcatc aatgggaaat cccattcacc atcttcagg 300
gagcgagatc cctccaaaat tcaagtgggg ggcgatgctg ggcgcttgag ttacgttcgt 360
gggagtcca ctgggccttc tttcaaccac ccttgagaga gggtttgggg gttcattttt 420
caaggggggg gagcccaaan ggtcttcat tttttggccc cttttt 467
```

&lt;210&gt; 168

&lt;211&gt; 316

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(316)

&lt;223&gt; 3' terminal sequence. desmin (DES) gene.

&lt;400&gt; 168

```
ggcttgtgtt tntntctctt ttattgtttc tctccagagc ccctgcagca ggggagggga 60
gggcgtgggg aggtgggggc cctcccacc agcctgagac cgctctctgc ctctctctc 120
tcctctcttc tccagcatct cac ccacttt ctctcttct naatctctg ctcccacctc 180
cagcaccttc ggggattccc tctttagacc cctgctttct aagtcacccc ggggctgggg 240
aaaggaaaat aagagaccac ggggacaatt tcaagcccc cagtntccac aggggctagt 300
ccctgggnt acctgc 316
```

&lt;210&gt; 169

&lt;211&gt; 440

&lt;212&gt; DNA

111/292

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(440)

&lt;223&gt; 5' terminal sequence. desmin (DES) gene.

&lt;400&gt; 169

```
atctcccat ccagacctac tctgccctca acttccgag a aaccagccct gagcaaaggg 60
gttctgaggt ccataccaag aagacggtga tgatcaagac catcgagaca cgggatgggg 120
aggtcgtcag tgaggccaca cagcagcagc atgaagtgt ctaaagacag agaccctctg 180
ccaccagaga ccgtcctcac ccctgtcctc actgctccct gaagccagcc ttcttccatc 240
ccagggacac cacacca gc cttcagtcct cccttcaca gctctggac ccctcctcac 300
tgggcatcct cctcgtggtt ccccaacagc ggacataggc ccatccttgc tgggttcaca 360
ggggcatggc cccgggccac ttnttgctgg aacccagtt gttgaggtt tgggtgtttg 420
ggcagttgag ttgaggtttt                                     440
```

&lt;210&gt; 170

&lt;211&gt; 2218

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2218)

&lt;223&gt; desmin (DES) gene.

&lt;400&gt; 170

```
cctcgccgca tccactctcc ggccggccgc ctgccgccg cctcctcc gt gcgccgccca 60
gcctcgcccg cgcgctcacc atgagccagg cctactctc cagccagcgc gtgtcctcct 120
accgccgcac ctccggcggc gcccggggt tcccgctcgg ctccccctg agctcgcccg 180
tgttcccgcg gccgggtttc ggtctaaagg gctcctccag ctccgtgacg tcccgctgtg 240
accaggtgtc gcgcacgtcg gccgggg ccg ggggcttggg gtcgtctgag gccagccggc 300
tggggaccac ccgcacgccc tcctcctacg gcgcaggcga gctgctggac ttctcactgg 360
ccgacgcggt gaaccaggag ttctgacca cgcgcaccaa cgagaagtg gagctgcagg 420
agctcaatga ccgcttcgcc aactacatcg agaaggtgcg ctccctggag cagcagaacg 480
cgctcgccgc cgaagtgaac cggtcaagg gccgcgagcc gacgcgagtg gccgagctct 540
acgaggagga gctgcgggag ctgcggcgcc aggtggaggt gctcactaac cagcgcgcgc 600
gcgtcgacgt cgagcgcgac aacctgctcg acgacctgca gcggctcaag gccagctgc 660
aggaggagat tcagttgaag gaagaagcag agaacaattt ggctgcc ttc cgagcggagc 720
tgatgcagc tactctagct cgcattgacc tggagcgcag aattgaatct ctcaacgagg 780
agatcgcggt ccttaagaaa gtgcatgaag aggagatccg tgagttgcag gctcagcttc 840
aggaacagca ggtccagggt gagatggaca tgtctaagcc agacctcact gccgccctca 900
gggatatccg ggctcagtat gagac catcg cggctaagaa cattcttgaa gctgaggagt 960
ggtacaagtc gaaggtgtca gacctgacct aggcagccaa caagaacaac gacgccctgc 1020
gccaggccaa gcaggagatg atggaatacc gacaccagat ccagtcctac acctgcgaga 1080
ttgacgccct caagggcact aacgattccc tgatgaggca gatgcgggaa ttggaggacc 1140
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ggcacctcaa ggtgagatg gcccgccatc tgcgcgagta ccaggacctg ctcaacgtga 1260
agatcgccct ggatgtggag attgccacct accggaagct gctggaggga gaggagagcc 1320
ggatcaatct ccccatccag acctactctg ccctcaactt ccgagaaacc agccctgagc 1380
aaaggggttc tgaggtccat accaagaaga cgggtgatgat caagaccatc gagacacggg 1440
atggggaggt cgtcagtgag gcgacacagc agcagcatga agtgctctaa agacgagaga 1500
ccctctgccca ccagagaccg tcctcaccct tgcctcact gctcctgaa gccagcctt 1560
```



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```

cttccatccc agga caccac acccagcctc agtcctcccg tcacagcctc tgaccctcc 1620
tcactggcca tcctcgtgg tcccaacag cgacatagcc catccctgcc tggtcacagg 1680
catgccccgg ccacctctgc ggaccccagc tgtgagcctt ggctgttggc agtgagttag 1740
cctggctott gtgtggatg gagcccaggc gggagcgggtg gccctgtccc tcc cacctct 1800
gtgacctgag gcctacgctt tggctctgga gatagcccca gagcaggggtg ttgggatact 1860
gcagggccag gactgagccc cgcagacctc cccagcccct agcccaggag agagaaagcc 1920
aggcaggtag cctgggggac tagccctgtg gagactgggg ggcttgaaat tgtccccgtg 1980
gtctcttact ttcctttccc cagcccag gg tggacttaga aagcaggggc tacaagaggg 2040
aatccccgaa ggtgctggag gtgggagcag gagattgaga aggagagaaa gtgggtgaga 2100
tgctggagaa gagagaggag gagagaggca gagagcggtc tgaggctggt gggaggggag 2160
cccacctccc cagccctcc cccccctgc tgcaggggct ctggagagaa acaataaa 2218

```

&lt;210&gt; 171

&lt;211&gt; 367

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(367)

&lt;223&gt; 5' terminal sequence. casein kinase 2, beta polypeptide (CSNK2B) gene.

&lt;400&gt; 171

```

gatccacgac cgctacatcc ttaccaaccg tggcatcgcc agatgttggg aaagtaccag 60
caaggagact ttggttactg tcctcgtgtg tactgtgaga accagccaat gcttcccatt 120
ggcctttcag acatcccagg tgaagccatg gtgaagctct actgcccac gtgcatggat 180
gtgtacacac ccaagtcacg aagacacatc cacacggatg ggcgcctac t ttcggcactg 240
gtttccctca catgctcttc atgggtgcat cccgagtacc ggcccagggt gaccttgcca 300
accagtttgt gccaggggtt ttacggtttt caaggttcca tncggtgggg cttaccagggt 360
tgcagggt
367

```

&lt;210&gt; 172

&lt;211&gt; 1128

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1128)

&lt;223&gt; casein kinase 2, beta polypeptide (CSNK2B) gene.

&lt;400&gt; 172

```

gcttctcggt gtgccccgcc cgcaagcgcc ctctccggg ccttc gtgac agccagggtg 60
tgcgcggtgc atcctgggat tggtagttcg ctttctctca tttagccagt ttctttctct 120
accggggact ccgtgtcccg gcatccaccg cggcacctga cccttgccgc ttgcgtgttg 180
ccctcttccc caccctccct aatttcact cccccaccc cacttcgct gccgcggtcg 240
ggtccgcggc ctgcgtgtga gcgg tcgccg ccgttccctg gaagtagcaa cttccctacc 300
ccacccagct cctgggtccc gtccagccgc tgacgtgaag atgagcagct cagaggaggt 360
gtcctggatt tcctggttct gtgggtccg tggcaatgaa ttcttctgtg aagtggatga 420
agactacatc caggacaaat ttaattctac tggactcaat gagcaggtcc ctcactatcg 480
acaagctcta gacatgatct tggacctgga gcctgatgaa gaactggaag acaaccccaa 540

```

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```
ccagagtgc ctgattgagc aggcagccga gatgctttat ggattgatcc acgcccgccta 600
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gtcatcaaga caccatcaca cggatggcgc ctacttcggc actggtttcc ctcacatgct 840
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ctacggtttc aagatccatc cg atggccta ccagctgcag ctccaagccg ccagcaactt 960
caagagccca gtcaagacga ttcgctgatt cctccccc cctgtcctgc agtctttgtc 1020
ttttcctttc ttttttgcca ccttttcagg aacctgtat ggtttttagt ttaaattaaa 1080
ggagtcgtta tcgtggtggg aatatgaaat aaagtagaag aaaaggcc 11 28
```

&lt;210&gt; 173

&lt;211&gt; 475

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(475)

<223> 3' terminal sequence. golgi apparatus  
protein 1 (GLG1) gene.

&lt;400&gt; 173

```
gggttttttt ctnaaaaaaa cctttgagtt gcaggtcagg tnagttgggt ctggaagtac 60
cggaagtctt gttggnatga gagagacttg tctacaggca gnaaaaccca agtttgccaa 120
acaaaggcag taaccccagc gaccagctgc tgctgctgca cgggtgaggag gaggaggaca 180
ccatggacac gagtggaggc tggatgggac aacgcagtgg acatctgcta atg ctctaac 240
acgggggttg ngtcacttct gagaagagcg aggttagtgg ggatnctata caagagggct 300
ntacaaactg gggcactggg atagggtagt tcctttgggn gggccaaggt gggctctacc 360
ccgtcctttg agctctngtg tncactnccg ttgggggatc cntcccaca cattcagggc 420
cantcaggna caattttacc aggtgntccc a ctgtttcac agggggattt aagtt 475
```

&lt;210&gt; 174

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(483)

<223> 5' terminal sequence. golgi apparatus  
protein 1 (GLG1) gene.

&lt;400&gt; 174

```
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gctgcactgc tcagacgaga tctccagtct atgtgctgaa gaagcagcag cccaagagca 180
gacaggtcag gtggaggagt gcc tcaaggt caacctgtc aagatcaaaa cagaattgtg 240
taaatnggaa gtgctaaaca tgctgaagga aagcaaaagca gacatctttg ttgacccggg 300
acttcatact tgcttgtgcc ctgggacatt aaacaccact gcgcagcatt caccctgggc 360
cgcgggcggt caaattgttc ctgtnttcat ggggaaggcac tgggaggggt aaggcgggtt 420
gaggtttaca gcccaggttg caaaaaggcg cttcattgac ccggtttgag gtgttggtt 480
ttt 483
```

<210> 175  
<211> 3909  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc feature  
<222> (1)..(3909)  
<223> golgi apparatus protein 1 (GLG1) gene.

<400> 175  
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ccagggcgctc ccac agccag ggccagggtc cgggggcca ctttgtgtcc ttcgtagggc 180  
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ttcagcagca acagcagcag cagcaacagc aacagcagcc tcagccgccc cagccgcctt 300  
tcccggcggg tgggcctccg cggcggggag gagcgggggc tgggggggc tggaag ctgg 360  
cggaggaaga gtcctgcagg gaggacgtga cccgcgtgtg ccctaagcac acctggagca 420  
acaacctggc ggtgctcgag tgcctgcagg atgtgagggg gcctgaaaat gaaatttctt 480  
cagactgcaa tcatttgttg tggaattata agctgaacct aactacagat cccaaatttg 540  
aatctgtggc cagagaggtt tgcaaatcta ctat aacaga gattaaagaa tgtgctgatg 600  
aaccggttgg aaaaggttac atggtttcct gcttagtgga tcaccgaggc aacatcactg 660  
agtatcagtg tcaccagtac attaccaaga tgacggccat catttttagt gattaccgtt 720  
taatctgtgg cttcatggat gactgcaaaa atgacatcaa cattctgaaa tgtggcagta 780  
ttcggcttgg agaaaaggat gcacattcac aagggtgagg gtatcatgc ttggagaaaag 840  
gcctggtgaa agaagcagaa gaaagagaac ccaagattca agtttctgaa ctctgcaaga 900  
aagccattct cgggttggct gagctgtcat cggatgactt tcaacttagac cggcatttat 960  
attttgcttg ccgagatgat cgggagcgtt tttgtgaaaa tacacaagct ggtg agggca 1020  
gagtgtataa gtgcctcttt aaccataaat ttgaagaatc catgagttaa aagtgtcgag 1080  
aagcacttac aaccgcccaa aagctgattg ccaggatta taaagtcagt tattcattgg 1140  
ccaaatcctg taaaagtgc ttgaagaaat accggtgcaa tgtggaaaac cttccgcgat 1200  
cgcgtgaagc caggctctcc tacttgta a tgtgcctgga gtcagctgta cacagagggc 1260  
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acttttctct gagccctgag atcatcctaa gctgtcgggg ggagattgaa caccattgtt 1380  
ccggattaca tcgaaaagga cggaccctac actgtctgat gaaggtagtt cgaggggaga 1440  
aggggaacct tggaatgaac tgccagcagg cgcttcaaac actgattcag gagactgacc 1500  
ctggtgcaga ttaccgcatt gatcgagctt gaatgaagc ttgtgaatct gtaatccaga 1560  
cagcctgcaa acatataga tctggagacc caatgatctc gtcgtgcctg atggaacatt 1620  
tatacacaga gaagatggta gaagactgtg aacaccgtct ct tagagctg cagtatttca 1680  
tctcccgga ttggaagctg gaccctgtcc tgtaccgcaa gtgccaggga gacgcttctc 1740  
gtctttgcca caccacgggt tggaatgaga ccagtgaatt tatgcctcag ggagctgtgt 1800  
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agtgcgcagc tgaagtc caa aggatcctac accagcgtgc catggatgtc aagctggatc 1920  
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ctggacagga gctggagtgc cttcaggacc atctggatga cttgggtgtg gagttagag 2040  
atatagttgg caacctcact gagttagaat cagaggatat ccaaatagaa gccttg ctga 2100  
tgagagcctg tgagcccata attcagacat tctgccacga tgcggataac cagatagact 2160  
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gtgccatcgg agttaccac ttccagctgg tgcagatgaa ggattttcgg ttttcttaca 2280  
agtttaaaat ggcctgcaag gaggacgtgt tgaagctttg cccaaacata aaaaagaagg 2340  
tggacgtggg gatctgcctg agcacgaccg tgcgcaatga cactctgcag gaagccaagg 2400  
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gttccgctgt gcaatatggc aacgctcaga ttatcgaatg tctgaaagaa aacaagaagc 2580  
agctaagcac ccgctgccac caaaaagtat ttaagctgca ggagacagag atgatggacc 2640  
cagagctaga ctacacctc atgaggggtct gcaagcagat gataaagagg ttctgtccgg 2700

115/292

```
aagcagattc taaaaccatg ttgcagtgc tgaagcaaaa taaa aacagt gaattgatgg 2760
atcccaaatg caaacagatg ataaccaagc gccagatcac ccagaacaca gattaccgct 2820
taaaccccat gttaagaaaa gcctgtaaag ctgacattcc taaattctgt cacggatatcc 2880
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gatatgctga ccagcgccct g tcttcagact gtgaagacca gatccgaatc attatccagg 3000
agtcgccct ggactaccgc ctggatcctc agctccagct gcaactgctca gacgagatct 3060
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tgaaggaaag caaacgagac atctttgttg acccggtact tcatactgct tgtgccctgg 3240
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tgcttttgtt tggcaaacct gggtttacct gcctgtagac aagtct ctct cataccaaca 3840
gaacttcggt tacttcaga accaactcac ctgacctgca actcaaaggc tttttaaga 3900
aaaccacca                                     3909
```

&lt;210&gt; 176

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(390)

<223> 5' terminal sequence. endothelin receptor  
type b (EDNRB) gene.

&lt;400&gt; 176

```
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tttgaatctg tcattcacat accctgtgaa gac aatacta tctacaattt tttcaggatt 120
attaaaatct tcttctttca ctatcgtagc ttaaactctg tttggttttg tcatctgtaa 180
atacttaoct acatacactg catgtagatg attaaatgag ggcaggccct gtgctcatag 240
ctttacgatg gagagatgcc agtgacctca taataaagac tgtggaactg cctgggtgca 300
gtgtccacat gacaaagggg caggtaggca ccctctcttc acctatgctg tgggttaaat 360
gggtttctag gcataatgat tatggctatt                                     390
```

&lt;210&gt; 177

&lt;211&gt; 4286

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4286)

&lt;223&gt; endothelin receptor type b (EDNRB) gene.

&lt;400&gt; 177

gagacattcc ggtgggggac tctggccagc ccgagcaacg tggatcctga gagcactccc 60  
 aggtaggcat ttgccccggt gggacgcctt gccagagcag tgtgtggcag gcccccgtgg 120  
 aggatcaaca cagtggctga ac actgggaa ggaactggta cttggagtct ggacatctga 180  
 aacttggctc tgaactgcg cagcgccac cggacgcctt ctggagcagg tagcagcatg 240  
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 accgcagaga taatgacgcc acccaactaag accttatggc ccaagggttc caacgccagt 420  
 ctggcgcggt cggtggcacc tgcggagggt cctaaaggag acaggacggc aggatctccg 480  
 ccacgcacca tctccccctc ccgcgtgcaa ggaccatcg agatcaagga gacttttcaa 540  
 tacatcaaca cggttgtgtc ctgccttgtg ttctgtgtgg gg atcatcgg gaactccaca 600  
 ctctctgaga ttatctacaa gaacaagtgc atgcgaaacg gtcccaatat cttgatcgcc 660  
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 ctgctggcag aggactggcc atttggagct gagatgtgta agctgggtgcc tttcatacag 780  
 aaagcctccg tgggaatcac tgtgctgagt ctatgtgtc tgagtattga cagatatcga 840  
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 ttctgcttgc cattggccat cactgcattt tttatacac taatgacctg tgaatgttg 1140  
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 gccaaaaccg tcttttgctt ggtccttgtc tttgccc tct gctggcttcc ccttcacctc 1260  
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 taaaatatta agtgaatta ttttaacact cacagctaca tatgacattt tatgagctgt 1740  
 ttacggcatg gaaagaaaat cagtgggaat taagaaagcc tgcgtgtgaa agcacttaat 1800  
 tttttacagt tagcacttca acatagctct taacaacttc caggatattc acacaacact 1860  
 taggcttaaa aatgagctca ctacg aattt ctattcttcc taaaaagaga tttattttta 1920  
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 aagcttaaat tactcaattt aaaattttta aatcctttta aacaactttt caattaatat 2040  
 tatcacacta ttatcagatt gtaattagat gcaaatgaga gagcagttta gttgttgcatt 2100  
 ttttcggaca ctggaaacat ttaaatgatc aggaaggagt aacagaaaga gcaaggctgt 2160  
 ttttgaaaat cattacactt tcaactagaag cccaaacctc agcattctgc aatatgtaac 2220  
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 tataatactt ttaaaaagaa aattattaca tcttttaca t tcaagttaaga tcaaacctca 2340  
 caaagagaaa tagaatgttt gaaaggctat cccaaaagac ttttttgaat ctgtcattca 2400  
 catacctgt gaagacaata ctatctacaa ttttttcagg attattaaaa tcttcttttt 2460  
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 taaagcttat tactaatttt tgtattattt ttgtaaatag ccaatagaaa agtttgcttg 2820  
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 agcttttgct gttcctgcct aatttttata tcttctaagc aaagtgcctt aggatagctt 2940  
 gggatgagat gtgtgtgaaa gtatgta caa gagaaaacgg aagagagagg aaatgaggtg 3000  
 gggttggagg aaacccatgg ggacagattc ccattcttag cctaacgttc gtcattgcct 3060  
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 gagtgaactt cgaaataaat tgggccaag agctttaact cggctcttaa atatgccaa 3180  
 atttttactt tgtttttctt ttaataggct gggccacatg ttggaaataa gctagtaagt 3240  
 ttgttttctg tcaattatga atgtgatggt acagtaaacc aaaaccaac aatgtggcca 3300  
 gaaagaaaga gcaataataa ttaattcaca caccatattg attctattta taaatcacc 3360  
 acaacttgt tctttaattt catcccaatc actttttcag aggcctgtta tcatagaagt 3420  
 cattttagac tctcaatttt aaattaattt tgaatcacta atattttcac agtttattaa 3480  
 tatatttaatt ttctatttaa atttttagatt atttttatta ccatgtactg aatttttaca 3540  
 tctgtatacc ctttcttctt ccatgtcagt atcatgttct ctaattatct tgccaaattt 3600  
 tgaaactaca caca aaagc atacttgcatt tatttataat aaaattgcat tcagtggctt 3660

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tttaaaaaaa atgtttgatt caaaacttta acatactgat aagtaagaaa caattataat 3720
ttctttacat actcaaaacc aagatagaaa aagggtgctat cgttcaactt caaaacatgt 3780
ttcctagtat taaggacttt aatatagcaa cagacaaaat tattgttaac atgg atgtta 3840
cagctcaaaa gatttataaa agattttaac ctattttctc ccttattatc cactgctaata 3900
gtggatgtat gttcaaacac ctttttagtat tgatagctta catatggcca aaggaatata 3960
gtttatagca aaacatgggt atgctgtagc taactttata aaagtgtaat ataacaatgt 4020
aaaaaattat atatctggga ggatttttt g gttgcctaaa gtggctatag ttactgattt 4080
tttattatgt aagcaaaacc aataaaaatt taagtttttt taacaactac cttatttttc 4140
actgtacaga cactaattca ttaaatacta attgattgtt taaaagaaat ataatgtga 4200
caagtggaca ttatttatgt taaatataca attatcaagc aagtatgaag ttattcaatt 4260
aaaatgccac atttctgggc tctggg 4286

```

&lt;210&gt; 178

&lt;211&gt; 462

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(462)

<223> 3' terminal sequence. gran zyme b (granzyme  
2, cytotoxic t-lymphocyte-associated serine  
esterase 1) (GZMB) gene.

&lt;400&gt; 178

```

acancagaga tccatttatt acagtctctgc aaccocgact gccaccacct tgggaattct 60
tgccctctgtc ccagagatgg tcaggcccag aggaagggtta gtctcatgcc tgctgttaga 120
ggcgnttcat tgttctcttt atccagggca ggaagntga gacctgatg tagactcctg 180
gggggtgtccc tttttgttt ccataggaga gaataccttg ggctangtcc ttacananga 240
ggggccccc ggagttcccc cttgaaaccg gtctgtgtct tctttggatc cccacacaa 300
atntcagtgg gctctgctgt aattgccatg ggaaggagac gggtcac ant gggcagttcc 360
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taaccocagg ccaggccaaa ttgaaaagtt gcctgggntt tt 462

```

&lt;210&gt; 179

&lt;211&gt; 960

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(960)

<223> granzyme b (granzyme 2, cytotoxic  
t-lymphocyte-associated serine esterase 1) (GZMB)  
gene.

&lt;400&gt; 179

```

agcagctoca accagggcag ctttctgag aagatgcaac caatcctgct tctgctggcc 60
ttcctcctgc tgcccagggc agatgcaggg gagatcatcg ggggacatga ggccaagccc 120
cactcccgcc cctacatggc ttatcttatg atctgggatc agaagtctct gaagagggtgc 180
ggtggcttcc tgatacaaga cgacttcgtg ctgacagctg ctactgttg gggaagctcc 240
ataaatgtca ccttgggggc ccacaatatc aaagaacagg agcc gaccca gcagtttatc 300
cctgtgaaaa gaccatccc ccatccagcc tataatccta agaacttctc caacgacatc 360

```

118/292

atgctactgc agctggagag aaaggccaag cggaccagag ctgtgcagcc cctcaggcta 420  
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acggccccc tgggaaaaca ct cacacaca ctacaagagg tgaagatgac agtgcaggaa 540  
gatcgaaagt gcgaatctga cttacgccat tattacgaca gtaccattga gttgtgcgtg 600  
ggggaccag agattaaaaa gacttccttt aagggggact ctggaggccc tcttgtgtgt 660  
aacaagggtg cccaggggcat tgtctcctat ggacgaaaca atggcatgcc tccacgagcc 720  
tgcaccaaag tctcaagctt tgtacactgg ataaagaaaa ccatgaaacg ctactaacta 780  
caggaagcaa actaagcccc cgctgtaatg aaacaccttc tctggagcca agtccagatt 840  
tacactggga gaggtgccag caactgaata aatacctctc ccagtgtaaa tctggagcca 900  
agtccagatt tacactggga gaggtgccag caactgaata aa tacctctt agctgagtgg 960

&lt;210&gt; 180

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(471)

<223> 3' terminal sequence. fibroblast growth  
factor receptor 1 (fms-related tyrosine kinase 2,  
pfeiffer syndrome) (FGFR1) gene.

&lt;400&gt; 180

tnaagcagca gcaattttta ttgagggacc taaactgaaa ataggttttag aacataatTT 60  
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&lt;210&gt; 181

&lt;211&gt; 463

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(463)

<223> 5' terminal sequence. fibroblast growth  
factor receptor 1 (fms-related tyrosine kinase 2,  
pfeiffer syndrome) (FGFR1) gene.

&lt;400&gt; 181

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aacacaaatg tattaatctg agtatatatt ttacatgtnt ttt

463

&lt;210&gt; 182

&lt;211&gt; 4066

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4066)

&lt;223&gt; fibroblast growth factor receptor 1

(fms-related tyrosine kinase 2, pfeiffer syndrome)

(FGFR1) gene.

&lt;400&gt; 182

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<210> 183

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(415)

<223> 5' terminal sequence. protein phosphatase 2  
(formerly 2a), catalytic subunit, alpha isoform  
(PPP2CA) gene.

<400> 183

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ccccaccac cacggctcatc tggatctgac cacagcaagt cacacattgg accctcatgg 180
ggaacttctt gtaggcgac aagtgtctctg atatgatcca gtgtat ctat agatggcgag 240
agaccaccat gtagacagaa gatctgcccc tccaccaagg cagtgaagg aagatagtca 300
aaaagatctg taaaatattt ccaaacattt ggcatttcca tattttctta aacattcatt 360
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<210> 184

<211> 2181

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

121/292

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2181)

<223> protein phosphatase 2 (formerly 2a),  
catalytic subunit, alpha isoform (PPP2CA) gene.

&lt;400&gt; 184

```
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tactgcggtg agagccagcg ggccagcgcc agcctcaaca gccgccagaa gtacacgagg 120
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agacttaatt gtaaaacat ataacttgag atttaagtct ttgggttggt ttttaataaa 2160
acagcatgtt ttcaggtaga g 2181
```

&lt;210&gt; 185

&lt;211&gt; 375

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(375)

<223> 5' terminal sequence. homo sapiens, clone  
image:4054156, mrna, partial cds (EST R55460)  
gene.

122/292

<400> 185  
cgaagaggat gaggaagagc tntctgtgct gcancaagag ctccaggccg ggctgcgcac 60  
caaggccctg attgtggatg agtcctgccg gcggtnacca tcttccaaca tagggatata 120  
cctccctcct tcttataact gaagatcctg gagcccgaa gattcag ggc agacagaccc 180  
tgataatgag cctggcaggg aagggaacc aacatcttgt aacttgcttt cccaccctg 240  
tttctggggg cagagcaatt gcccaatttc taccctaate caaagtcctt ggggtgnggt 300  
gggggttaaac gtgctgggtgc atcctaggtc atccaagagt gaggcgcaa gttcctgagg 360  
aagggggcac agaac 375

<210> 186

<211> 542

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(542)

<223> 3' terminal sequence. immunoglobulin kappa  
constant (IGKC) gene.

<400> 186  
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tggggataga agttttttca gcaggcacac aacagaggca nttccagatt tncaactgct 480  
catcagatgg ccgggaagnt gaaggncagt nggtgcagcc acattncttt tgatccncca 540  
ct 542

<210> 187

<211> 296

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(296)

<223> 5' terminal sequence. melanocortin 1  
receptor (alpha melanocyte stimulating hormone  
receptor) (MCLR) gene.

<400> 187

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acatctccat cttctacgca ctgnctacca cagcatcgtg accctgccgc gggcgcgaa 120  
nccgttgccg ccatctgggt ggccagtgtc gtcttcagca cgctcttcat cgcctactac 180  
gaccagtgg ccgtcctgct gtgcctcgtg gtcttcttcc tggctatgct ggtgctcatg 240  
gccgtgctgt acgtccacat gctggccccg gcctgccagc acgccaggg cattcg 296

<210> 188

123/292

<211> 1270  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1270)  
<223> melanocortin 1 receptor (alpha melanocyte  
stimulating hormone receptor) (MC1R) gene.

<400> 188  
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<210> 189  
<211> 336  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(336)  
<223> 3' terminal sequence. neuregulin 1 (NRG1)  
gene.

<400> 189  
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gaatgaattg aatcgaaaaa nncannccac aaaatt 336

124/292

<210> 190  
<211> 366  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(366)  
<223> 5' terminal sequence. neuregulin 1 (NRG1)  
gene.

<400> 190  
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gttcagaccg aagctctgcc agagacggtc atgcagcttt ttccgctgtt tcttggtttt 180  
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gggcac 366

<210> 191  
<211> 2490  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2490)  
<223> neuregulin 1 (NRG1) gene.

<400> 191  
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gatacaaaaa aagccaggga agtcag aact tcgcattaac aaagcatcac tggttgattc 780  
tgagagagat atgtgcaaag tgatcagcaa attaggaaat gacagtgcct ctgccaatat 840  
caccatcgtg gaatcaaacg agatcatcac tggatgccca gcctcaactg aaggagcata 900  
tgtgtcttca gagtctccca ttagaatatc agtatccaca gaaggagcaa atacttcttc 960  
atctacatct acatccacca ctgggacaag ccactttgta aaatgtgcgg agaaggagaa 1020  
aactttctgt gtgaatggag gggagtgtt catggtgaaa gacctttcaa acccctcgag 1080  
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cagcttctac aaggcggagg agctgtacca gaagagagt ctg accataa ccggcatctg 1200  
catcgccctc cttgtggtcg gcatcatgtg tgtggtggcc tactgcaaaa ccaagaaaca 1260  
gcggaataag ctgcatgacc gtcttcggca gagccttcg tctgaacgaa acaatatgat 1320  
gaacattgcc aatgggcctc accatcctaa cccaccccc gagaatgtcc agctggtgaa 1380

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```

tcaatacgtat tctaaaaa cg tcactctccag tgagcatatt gttgagagag aagcagagac 1440
atcctttttcc accagtcact atacttccac agcccatcac tccactactg tcaccagac 1500
tcctagccac agctggagca acggacacac tgaaagcatc ctttccgaaa gccactctgt 1560
aatcgtgatg tcatccgtag aaaacagtag gcacagcagc ccaactgggg gcccaag agg 1620
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aaccctgat tcctaccgag actctcctca tagtgaaagg tatgtgtcag ccatgaccac 1740
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ggaaatgtct ccaccggtgt ccagcatgac g gtgtccaag ccttccatgg cggtcagccc 1860
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gtttgaccat caccctcagc agttcagctc ctccaccac aaccocgcgc atgacagtaa 1980
cagcctccct gctagcccct tgaggatagt ggaggatgag gagtatgaaa cgacccaaga 2040
gtacgagcca gcccaagagc ctgttaagaa actcgccaat agccggcggg ccaaaagaac 2100
caagccaat ggccacattg ctaacagatt ggaagtggac agcaacacaa gctcccagag 2160
cagtaactca gagagtgaaa cagaagatga aagagtaggt gaagatacgc ctttcctggg 2220
catacagaac cccctggcag ccagtcttga ggcaacacct gcctt ccgcc tggctgacag 2280
caggactaac ccagcaggcc gcttctcgac acaggaagaa atccaggcca ggctgtctag 2340
tgtaattgct aaccaagacc ctattgctgt ataaaaccta aataaacaca tagattcacc 2400
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ttagcagttc tgcaataaaa aaaaaaaaaa 2490

```

&lt;210&gt; 192

&lt;211&gt; 453

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(453)

&lt;223&gt; 5' terminal sequence. ciliary neurotrophic factor receptor (CNTFR) gene.

&lt;400&gt; 192

```

cagatgctac gccgggaagg agtacattat ccagggtggca gccaaaggaca atnagattgg 60
gacatggagt gactggagcg taccgcccac gctacgccct ggactgagga accgcgacac 120
ctcaccacgg aggccaggc tgcgagagacc acgaccagca ccaccagctc cctggcaccc 180
ccacctacca cgaagatctg tgaccctggg gagctgggca gcggcggggg accctcggca 240
cccttcttgg tcagcgctcc catcactctg gccctggctg ncgctgccgc cactgccagc 300
agtctcttga tctgagcccg gcaccccatg aggacatgca gagcacctgc agaggancag 360
gaggccggag cttgagcctt gtagaccccg gtttctattt t ncacacggg caggaggant 420
ttttgcattn tttttnagac acaatttttt gga 453

```

&lt;210&gt; 193

&lt;211&gt; 1566

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1566)

&lt;223&gt; ciliary neurotrophic factor receptor (CNTFR) gene.

&lt;400&gt; 193

126/292

```

gcggcgccag cggaggcgcc ggctccagcc ggcgcgccgc gaggctcggc ggtgggatcc 60
ggcgggcggt gctagctccg cgctccctgc ctgctcgtc gccggggcg gtcggaaggc 120
gcggcgccgaa gcccgggtgg cccgagggcg cgactct agc cttgtcacct catcttgccc 180
ccttggtttt ggaagtccctg aagagtttgt ctggaggagg aggaggacat tgatgtgctt 240
ggtgtgtggc cagtgttgaa gagatggctg ctctgtccc gtgggcctgc tgtgtgtgc 300
ttgcgcgcgc cgccgcagtt gtctacgcc agagacacag tccacaggag gcaccccatg 360
tgcagtacga gcgcc tgggc tctgacgtga cactgccatg tgggacagca aactgggatg 420
ctgcggtgac gtggcggtg aatgggacag acctggcccc tgacctgtc aacggctctc 480
agctggtgct ccatggcctg gaactgggcc acagtggcct ctacgcctgc ttccaccgtg 540
actcctggca cctgcgccac caagtccctg tgcagtggg cttgccgcgc cgggagc ctg 600
tgctcagctg ccgctccaac acttacccca agggcttcta ctgcagctgg catctgcccc 660
ccccaccta cattcccaac accttcaatg tgactgtgct gcattggctc aaaattatgg 720
tctgtgagaa ggacccagcc ctcaagaacc gctgccacat tcgctacatg cacctgttct 780
ccaccatcaa gtacaaggtc tccataagtg tcagc aatgc cctggggccac aatgccacag 840
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agacacaatt tgtggagacc ccggcgggcc cgggcctgcc gccccccagc cctgccgcac 1560
caagct 1566

```

&lt;210&gt; 194

&lt;211&gt; 349

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(349)

<223> 5' terminal sequence. angiogenin,  
ribonuclease, rnase a family, 5 (ANG) gene.

&lt;400&gt; 194

```

ccgtgtacac aactcacac aaggacgcca accccaccta gatgcaaaga ggattcaaaa 60
gaacatcttt gcgttttcta ccggtccccc atcatcgtac tagggaggaa gaagcgggtg 120
agaaacaaaa cttctttcca ttgtcctgcc cgtttctgcg gacttgttct gaggccgagg 180
agcctgtggtt ggaagagatg gtgatgggcc tgggcgtttt gttgttggtc ttctgtgctg 240
gtctgggtct gacccaccg accctggctc aggataactn c aggtacaca cacttctga 300
cccagcacta tgatgccaaa ccacagggcc ngggatgaca gatactgtg 349

```

&lt;210&gt; 195

&lt;211&gt; 729

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

127/292

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(729)

<223> angiogenin, ribonuclease, rnase a family, 5  
(ANG) gene.

&lt;400&gt; 195

```
atgatgccgt gtcagagagc aaagctcctg tccttttggc ctaatttggg gatgctgttc 60
ttgggtctac cacacctcct tttgccctcc gcaggagcct gtgttggaag agatgggtgat 120
gggcctgggc gttttgttgt tggctctcgt gctg ggtctg ggtctgacct caccgacct 180
ggctcaggat aactccaggt acacacactt cctgacctag cactatgatg ccaaaccaca 240
gggccgggat gacagatact gtgaaagcat catgaggaga cggggcctga cctcaccctg 300
caaagacatc aacacattta ttcatggcaa caagcgcagc atcaaggcca tctgtgaaaa 360
caagaatgga aa ccctcaca gagaaaacct aagaataagc aagtcttctt tccagggtcac 420
cacttgcaag ctacatggag gttccccctg gcctccatgc cagtaccgag ccacagcggg 480
gttcagaaac gttgtgtgtg cttgtgaaaa tggcttacct gtccacttgg atcagtcaat 540
tttccgtcgt ccgtaaccag cgggccccctg gtcaagtgtt ggctctgctg tctt tgcctt 600
ccatttcccc tctgcacca gaacagtggg ggcaacattc attgccaagg gcccaaagaa 660
agagctacct ggaccttttg tttctgtttt gacaacatgt ttaataaata aaaatgtctt 720
gatatcagt                                     729
```

&lt;210&gt; 196

&lt;211&gt; 452

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(452)

<223> 3' terminal sequence. endoglin  
(osler-rendu-weber syndrome 1) (ENG) gene.

&lt;400&gt; 196

```
ngttactcca gccttggacc ggggctgcc a tt ggagagn cgtggcgacc acaaggaggc 60
gcacatcctg agggtcctgc cgggcoactc ggcgggcccc ggacgggtga cgggtgaagg 120
ggaactgagc tgcgaccccg gggatctcga tgccgtcctc atoctgcagg gtccccctta 180
cgtgtcctgg ctcatcgacg ccaaccacaa catgcagatc tggaccactg gagaatactc 240
cttcaagatc tttccagaga aaaacattcg tggcttcaag ctcccagaca cacctcaagg 300
cctcctgggg ggacgcgngn atgcttcaat gccagcattg tggcatcctt cgtgggagct 360
taccgtggg ccagcattgt cttnatttca ttgccttcca gcttgcggtt gttagggttg 420
cagaccttaa cccgnaccgt ttccagacca tt                                     452
```

&lt;210&gt; 197

&lt;211&gt; 379

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(379)

<223> 5' terminal sequence. endoglin  
(osler-rendu-weber syndrome 1) (ENG) gene.

&lt;400&gt; 197



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aggacgagc ctttgcttgt gcaaccagac aggtcagggc tgatgatgtt caagcgcatg 60  
aagacagtcc tatggcttcc tggctttgag acccgttctt gggacgcagg gctaccgtgc 120  
agctgagggt gccggttttg ggtatgggta ctgtgtagaa gtggaggagg aagctgaagc 180  
gcgggtcacc ctcggggctt ggggacagca ggct cacaca gttgcccttg gccgcccgcc 240  
cctgggatga gttccacggg gcctccctca ggccccaagt ccagggtggc agctgtctaa 300  
ctggagcagg aactcggaga cggatgggga cantctgacc tgcacaaagc tttntttgcc 360  
ccggcttcga tgggttttt 379

&lt;210&gt; 198

&lt;211&gt; 3142

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3142)

<223> endoglin (osler-rendu-weber syndrome 1)  
(ENG) gene.

&lt;400&gt; 198

cctgggcccgc ccgggctgga tgagccgg ga gctccctgct gccggtcata ccacagcctt 60  
catctgcgcc ctggggccag gactgtgct gtcactgcc tccattggag ccacagcacc 120  
cctccccgcc catccttcgg acagcaactc cagcccagcc ccggtccct gtgtccactt 180  
ctcttgacc ctcgcccgcc acccagaag gctggagcag ggacgcgctc gctccggccg 240  
cctgtctccc tcgggtcccc gtgcgagccc acgccggccc cgtgcccgc ccgcagccct 300  
gccactggac acaggataag gccacgcga caggcccca cgtggacagc atggaccgcg 360  
gcacgctccc tctggctgtt gccctgctgc tggccagctg cagcctcagc cccacaagtc 420  
ttgcagaaac agtccattgt gaccttcagc ctgtgggccc cgagagggg c gaggtgacat 480  
ataccactag ccaggctctg aagggtgctg tggctcaggc ccccaatgcc atccttgaag 540  
tccatgtct cttcctggag ttcccaacgg gcccgtcaca gctggagctg actctccagg 600  
catccaagca aaatggcacc tggcccgag aggtgcttct ggtcctcagt gtaaacagca 660  
gtgtcttct gcatctccag gccctgg gaa tccactgca cttggcctac aattccagcc 720  
tggtcacett ccaagagccc ccgggggtca acaccacaga gctgccatcc ttcccaaga 780  
cccagatcct tgagtggca gctgagagg gccccatcac ctctgtgct gagctgaatg 840  
accccagag catcctctc cgactggcc aagcccagg gtactgtcc ttctgcatgc 900  
tggaagccag ccaggacatg ggccgcagc tgcagtggcg gccggtact ccagccttg 960  
tccggggctg ccacttgaa ggctggccg gccacaagga ggccacatc ctgagggtcc 1020  
tgccgggcca ctggccggg ccccgagcg tgacgtgaa ggtggaactg agctgcgcac 1080  
ccggggatct cgatgcgctc ctcatctgc aggtccccc ctacg tgtcc tggctcatcg 1140  
acgccaacca caacatgcag atctggacca ctggagaata ctcttcaag atctttccag 1200  
agaaaaacat tctgtgcttc aagctcccag acacacctca aggcctctg ggggaggccc 1260  
ggatgctcaa tgccagcatt gtggcatcct tctgtgagct accgctggcc agcattgtct 1320  
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tcttgccag tgcctactcc agctgtggca tgcaggtgtc agcaagtatg atcagcaatg 1620  
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ccgagttct gctccagta gacagctgc acctggactt gggccctgag ggaggcaccg 1860  
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gcaaaggcct cgtcctgccc gccgtgctgg gcatcacctt tgggtgccttc ctcatcgggg 2160  
ccctgctcac tgtgcactc tggtagatct actgcacac gcgtgag tac cccaggcccc 2220

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```

cacagtgagc atgccgggcc cctccatcca cccgggggag ccagtgaa cctctgaggg 2280
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ccccagcaa ggggagccc gtggtggcgg tggctgcccc ggctcctcg gagagcagca 2400
gcaccaacca cagcatcggg a gacccaga gacccccctg ctccaccagc agcatggcat 2460
agccccggcc ccccgcgctc gccagcagg agagactgag cagccgccag ctgggagcac 2520
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tgaacctga aaaaaaaaaa aa 3142

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&lt;210&gt; 199

&lt;211&gt; 402

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(402)

<223> 3' terminal sequence. epidermal growth  
factor (beta-urogastrone) (EGF) gene.

&lt;400&gt; 199

```

tatgtttttg gtgattttat ttaaataatt agaagaaatt catcgttgtc tataatgaaa 60
acaaatcagg caatttactt acaatcttgt aactgaaaat acatacaaa t tctgtgcaat 120
cacaccaaga gggaaaattc tgtaggggaa aaggacagta atgactaaga aactccgaag 180
cctcctgtgt aatattttta aaataaaatg ttttcattca aatattttta aaaataagcc 240
atctaattct gaagaaatca gtttctaaat tacatttttc attgattcat cacaactcat 300
tttgcaaaat catcagcatg gaccacg cca atgaggagt aaatgcctac actgtatctt 360
aacggtattg taatattcca atcatttcat gaaactgata ta 402

```

&lt;210&gt; 200

&lt;211&gt; 4877

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4877)

<223> epidermal growth factor (beta-urogastrone)  
(EGF) gene.

&lt;400&gt; 200

```

actgtttggga gaggaatcgt atctccatat ttcttctttc agccccaatc caagggttgt 60
agctggaact ttccatcagt tcttcttttc ttttctctct ctaagccttt gccttgcctc 120
gtcacagtga agtcagcca g agcagggtg ttaaactctg tgaaatttgt cataagggtg 180
tcaggtatctt cttactggct tccaaagaaa catagataaa gaaatctttc ctgtggcttc 240

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ccttggcagg ctgcattcag aaggtotctc agttgaagaa agagcttggg ggacaacagc 300  
acaacaggag agtaaaagat gcccaggggc tgaggcctcc gctcaggcag ccgcatctgg 360  
gggtcaatcat actcaccttg cccggggccat gctccagcaa aatcaagctg ttttcttttg 420  
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agaaagacaa cttttgcaaa gagtttttct gaatgggtca aggcaagaga gagtatgtaa 780  
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ggtttatgcc ctgatcatg accctgtgga aaataagata tactttgccc atacagccct 2040  
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131/292

```

taagggtcc tgtccccagg taatggagcg aagctttcat atgccctcct atgggacaca 3960
gacccttgaa gggggtgtcg agaagcccca ttctctccta tcagctaacc cattatggca 4020
acaaagggcc ctggaccac cacac caaat ggagctgact cagtgaacac tgggaattaaa 4080
aggaaagtca agaagaatga actatgtcga tgcacagtat cttttctttc aaaagtagag 4140
caaaactata ggttttggtt ccacaatctc tacgactaat cacctactca atgcctggag 4200
acagatacgt agttgtgctt ttgtttgctc ttttaagcag tctcactgca gtottatttc 4260
caagtaagag tactgggaga atcactagggt aacttattag aaacccaaat tgggacaaca 4320
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aaaatcacca aaaacat
4877

```

<210> 201  
 <211> 153  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(153)  
 <223> 3' terminal sequence. hmt1 (hnrnp  
 methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)  
 gene.

```

<400> 201
attagacctc acattaggga aaacatcaaa atgancacg cagaccctt gagatcctga 60
ggttggccca gccgagcccg tgctcagaag cccccagct cgggccccca gctgcccga 120
cgcccgcct caccagcagg caggtoccca tcc
153

```

<210> 202  
 <211> 472  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(472)  
 <223> 5' terminal sequence. hmt1 (hnrnp  
 methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)  
 gene.

```

<400> 202
agtgaatcgc agggagaaga gcctgctgag tncagtgagg cgggtctcct gcaggaggga 60
gtacagccag aggagtttgt ggccatcgcg gactacgtg ccacgatga gaccagctc 120
agttttttga gaggagaaaa aattcttatc ctgagacaaa cactgcaga ttggtgttg 180
ggtgagcgtg cgggctgctg tgggtacatt c cggcaaac atgtggggaa gcacgtgat 240
gagtacgacc ccaggacac gtggcaggat gaagagtact tcggcagcta tggaaactctg 300

```

132/292

```

aaactccact tgggagatgt tggcagacca gccacgaaca actaaatacc acagtgttca 360
ttctctgncag gaattaaaga atccctgnac ggnttaaagt tcttcnnggg acgtggggct 420
gtgggggattt gggatccntc agtctcttnt tgttgacacat tttgcgtggc nt 472

```

&lt;210&gt; 203

&lt;211&gt; 2093

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2093)

<223> hmt1 (hmrnp methyltransferase, s.  
cerevisiae)-like 1 (HRMT1L1) gene.

&lt;400&gt; 203

```

cactgcgctt gcgcggggtt agggcgggtg ctcaagtctc tggaaaggac cgtccacccc 60
tccgcgctgg cgggtgtggac gcggaactca gcggagaaac gcgattgaga aatggaaaag 120
aaaatgaaat aaatcagcag ttatgaggca gagcctaaga gaactatggc aa catcaggt 180
gactgtccca gaagtgaatc gcaggagaaa gagcctgctg agtgacgtga ggcgggtctc 240
ctgcaggagg gactacagcc agaggagttt gtggccatcg cggactacgc tgccaccgat 300
gagaccacgc tcagtttttt gagaggagaa aaaattctta tcctgagaca aaccactgca 360
gattggtggt ggggtgagcg tgcgggctgc tgtgggtaca ttccggcaaa ccatgtgggg 420
aagcacgtgg atgagtaaga ccccgaggac acgtggcagg atgaagagta cttcggcagc 480
tatggaactc tgaactcca cttggagatg ttggcagacc agccacgaac aactaaatac 540
cacagtgtca tcctgcagaa taaagaatcc ctgacggata aagtcacctt ggacgtgggc 600
tgtgggactg ggatcatcag tctcttctgt gcacactatg cgcggcctag agcgggtgtac 660
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gtgccagtgg cgtgtaggga aactgcctt ggctcagcgt gcgagctaag gtggcgatgt 1980
atgcgatggg actctgcatg ggatagtaca gttgtgtaga cgtcttccaa ataaattatg 2040
tgttggtgcc atcgacatg ctcaataaat attttaaat agtgaaaaaa aaa 2093

```

&lt;210&gt; 204

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(431)

<223> 3' terminal sequence. ets variant gene 4  
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 204

```
tgggggcctt tatta aggtc tggcagatgt ggtggaggtg gaagtacaaa cccaggcctg 60
ggcctaggaa agggcagaag aaaggcaaag ggtcccttgg agcaggaacc catccctctc 120
tgcttatacc cagcaccctt catcccaggt tcctttcttc aacctccgcc tgctcttggg 180
aacacagagc accaagaact gacaaaccgg gaccctccag gggccacagc gtgggggc ag 240
agtccagggn ttctgtctcc ccgcagtggg gagatctngg ggagctcagg tgaacctcct 300
cancctcctg ccagtatgaa gttggggaag cgccttttct tgtccccag aacagaacaa 360
actcttgttc tctgtgggtt ngggggaaaa ggtttngggg ggtttggact taggggagaa 420
gttnagcttg a                                     431
```

<210> 205

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(435)

<223> 5' terminal sequence. ets variant gene 4  
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 205

```
gtccccctgcc cctgcccttg gacagtgcgc cctacagncc tttccccggg cagagaacgg 60
aatttcctga gatcctcttg cacctcccag cccaccctg gccatgggta cctcggggaa 120
catagctccg tcttcacga gcccctggga catttgccac tccttcacat ctcagggagg 180
gggccgggaa cccctcccag gcccctacc aacaccagct gtoggagccc tgcccaccct 240
atccccagca gagctttaag caagaatacc atgatcccct gtatggaaca gggnggggcc 300
agccaggccg tgggaaccag ggttgggggt tcaatggggg cacagggtac ccaggggggn 360
gggggggttg ttgattcaaa acagggaaca gacgggattt tt ggnttaag gatttnaggt 420
tntttaancg gggtg                                     435
```

<210> 206

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(447)

<223> 5' terminal sequence. annexin a11 (ANXA11)  
gene.

<400> 206

```

agacccagct cctctttgac atttatgaga taaaggaagc catcaagggg gttggcactg 60
atgaagcctg cctgattgag atcctcgctt cccgcagcaa tgagcacatc cgagaattaa 120
acagagccta caaagcagaa ttcaaaaaga ccctggaaga ggcca ttoga agcgacacat 180
cagggcactt ccagcggctc ctcatctctc tctctcaggg aaaccgtgat gaaagcacia 240
acgtggacat gtactcgcc cagagagatg cccaggagc tgtatgcggn ccggggagaa 300
ccgcctgggg aacagacgag tccaagtttc aattgcggtt tctgtggctt cccgggagcc 360
gggcncacc tgggtaggca gtt tttcaat gagttaccag agaatgnaca gggccnggac 420
attnntagaa gacatctgc ccggaga 447

```

&lt;210&gt; 207

&lt;211&gt; 1958

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1958)

&lt;223&gt; annexin all (ANXA11) gene.

&lt;400&gt; 207

```

gctgctgcgc ccgcggtctc ccagtgcctc gagtgcccg cgggccccgc gagcgggagt 60
gggacccagc cctaggcaga acccaggcgc cgcgcgccgg acgcccgcgg agagagccac 120
tcccgcacac gtccatttcc gcccctcgcg tccggagtcc ccgtggc cag atctaaccat 180
gagctaccct ggctatcccc cgcctccagg tggtaccaca ccagctgcac caggtggtgg 240
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aggggcctac cctgggcagc caccagtgc ctaccctgtt cagcctccag tgccactccc 660
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tcaccgtcct agagcttagg cctgtcttcc acccctcctg acccgatatg tgtgccacag 1860
gacctgggct ggctagaac tctctcaggc tgccctttct accccatccc tcacagcctc 1920
ttgctgctaa aatagatgtt tcatttttct gaaaaaaa 1958

```

&lt;210&gt; 208

&lt;211&gt; 433

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(433)

<223> 5' terminal sequence. platelet-derived  
growth factor receptor, beta polypeptide (PDGFRB)  
gene.

&lt;400&gt; 208

```
gccagatgaa gcaaggccat ataccctaaa cttccatcct gggggtcagc tnggctcctg 60
ggagattcca gatcacacat cacactctgg ggactcagga accatgcccc ttccccaggc 120
ccccagcaag tctcaagaac acagctgcac aggccttgac ttagagtnac agccggtntc 180
ctggnaaagcc cccagcagct gccccagga catgggaaga ccacgggacc tctttcacta 240
cccacgatga cctccggggg tatcctgggg caaaagggac aaagagggca aatgagatca 300
cctnctgcag cccaccactt ccagcacctg tgccgaggtt ttic gttcga agacagaatt 360
ggacagttga ggacagttat tgtctttntt taaaagnaca aggaagggtt cagnttgggt 420
taccaccaag gag                                         433
```

&lt;210&gt; 209

&lt;211&gt; 5570

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(5570)

<223> platelet-derived growth factor receptor,  
beta polypeptide (PDGFRB) gene.

&lt;400&gt; 209

```
ggcccctcag cctgtctgcc cagcacgagc ctgtgtctgc cctgccaac gcagacagcc 60
agaccaggg cgcccctct ggcggtctg ctctcccga aggatgcttg gggagtgagg 120
cgaagtggg cgtcctctc ccctacagca gccccttcc tccatccctc tgttctcctg 180
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atcccaccgt gggttcc tc cctaagtatg ccgaggaact attcatcttt ctacaggaaa 780
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137/292

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&lt;210&gt; 210

&lt;211&gt; 406

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(406)

<223> 5' terminal sequence. williams-beuren  
syndrome chromosome region 14 (WBSCR14) gene.

&lt;400&gt; 210

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gaccggcgta tcacacacat ctccgcgga caggagcggc gttcaacat caagctgggg 60
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aaagctacca cgctgcagaa gacagctgag tacatcctta tgctacagca ggagcgtgcg 180
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accagatgag agacatgttt gatggactac gtccgaaccc gtacgctgca caa ctgggaa 360
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&lt;210&gt; 211

&lt;211&gt; 3293

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3293)

<223> williams-beuren syndrome chromosome region  
14 (WBSCR14) gene.

&lt;400&gt; 211

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ccccgcgtg cgcggagcag ggaccaggcg gttgcggcgg cgacagccat ggccggcgcg 60
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aactcacac gcctcttcga gtgcttgagc ctggcctaca gtggcaagct ggtgtctccc 360
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gccatctgga gggcctggtg tatccagtat gtgaagcgga ggaagagccc cgtgtgtggc 480
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&lt;210&gt; 212

&lt;211&gt; 207

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(207)

&lt;223&gt; 5' terminal sequence. cd74 antigen

(invariant polypeptide of major histocompatibility complex, class ii antigen-associated) (CD74) gene.

<400> 212  
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ttccccagtc atcactcccc aaggaagagc caatgttttc cacccataat cttttctgcc 120  
gaccctagt tccctctgct cagccaagct tgttatcagc tttcagggcc atngttcaca 180  
ttagaataaa aggtagtaat taganaa 207

<210> 213  
<211> 1304  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1304)  
<223> cd74 antigen (invariant polypeptide of major  
histocompatibility complex, class ii  
antigen-associated) (CD74) gene.

<400> 213  
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tgaccagcgc gaccttatct ccaacaatga gcaactgccc atgctgggccc ggccgacctg 120  
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caagcctccc aagcctgtga gcaagatgcg catggccacc ccgtgtctga tgcaggcgct 360  
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cccctcccc atgtccacc ctgtacctca tcccatgaga cctgggtgcct ggctctttcg 840  
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ggaccataa tcctttctgc cgaccctag ttccctctgc tcagccaagc ttgttatcag 1260  
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<210> 214  
<211> 355  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(355)  
<223> 5' terminal sequence. annexin a7 (ANXA7)  
gene.

<400> 214  
aggaactatc cgaccagctg ccaacttcga tgctataaga gatgcagaaa ttcttcgtaa 60  
ggcaatgaag ggttttggga cagatgagca ggcaattgtn gatgtngttg ccaaccgttt 120  
ccaatgatca gaggcaaaaa attaaagcag catttaagac ctctatggc aaggatttaa 180  
tcaaagatct caaatcagag ttaagtngaa atatggaaga actgatcctn ggccctcttc 240  
atgcctccta cgtattacga tgctngagc ttacggaaa gcaatncagg gancaggta 300  
tcaggancgt tgtatttgat ttgngatttt ngtgcacang atcanattca ggtaa 355

<210> 215

<211> 2176

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2176)

<223> annexin a7 (ANXA7) gene.

<400> 215

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ggtcaggagt catcttttcc cccttctggt cagtatcctt atcctagtgg ctttcctcca 180  
atgggaggag gtgcctaccc acaagtgcc ahtagtggt acccaggagc tggaggtac 240  
cctgcgcctg gaggttatcc agccctgga ggctatcctg gtgcccaca gccaggggga 300  
gctccatcct atcccggagt tcctccaggc caaggatttg gagtcccacc agg tggagca 360  
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ccactacctg gtggttttcc tggaggacag atgccttctc agtatcctgg aggacaacct 480  
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<210> 216  
<211> 525  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(525)  
<223> 3' terminal sequence. thrombospondin 1  
(THBS1) gene.

<400> 216  
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tcatcttggt ctgtgacatg tggatggtgt gtgatcacia ggatccggct ctgcaactct 180  
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<210> 217  
<211> 5722  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(5722)  
<223> thrombospondin 1 (THBS1) gene.

<400> 217  
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143/292

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&lt;210&gt; 218

&lt;211&gt; 397

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(397)

<223> 3' terminal sequence. protein tyrosine  
phosphatase, non-receptor type 2 (PTPN2) gene.

&lt;400&gt; 218

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&lt;210&gt; 219

&lt;211&gt; 338

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(338)

<223> 5' terminal sequence. protein tyrosine  
phosphatase, non-receptor type 2 (PTPN2) gene.

&lt;400&gt; 219

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tctggcacct tctctctggt agacacttgt cttgttttga tggaaaaagg agatgatatt 120
aacataaaac aagtgttact gaac atgaga aaatacogaa tgggtcttat tcagacccca 180
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<210> 220

<211> 2287

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2287)

<223> protein tyrosine phosphatase, non -receptor  
type 2 (PTPN2) gene.

<400> 220

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<210> 221

<211> 296  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(296)  
<223> 3' terminal sequence. epha2 (EPHA2) gene.

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<210> 222  
<211> 3921  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3921)  
<223> epha2 (EPHA2) gene.

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<210> 223

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(437)

<223> 3' terminal sequence. tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1) gene.

<400> 223

```

ggaacagggt ggacactgtg caggcttcag ctccactcc gggcaggatt caggctatct 60
gggaccgcag gacttgccag gngcacagcc ctggctccc aggcaggcag gcaaggtgac 120
gggactggaa gcccttttca naggcttga ggagctggnc cgtccacaag caatgagtgc 180
cactctgcag tttgcagggg atggataaac agggaaacac tgtgcattcc tcacagccaa 240

```

cagtntaggt cttggtnaag ccccgcgct gagctaagct caggcttttc caggggagcc 300  
acgaaactnc aggtagtgat gtgcaagagt ccatcctgca gttttccagc aatnagaaac 360  
tcctcgttng cgggttttgg ggaccnttgg aagtntc cg cagacatttt tccatgggcc 420  
gggttttaag acgaacc 437

&lt;210&gt; 224

&lt;211&gt; 466

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(466)

<223> 5' terminal sequence. tissue inhibitor of  
metalloproteinase 1 (erythroid potentiating  
activity, collagenase inhibitor) (TIMP1) gene.

&lt;400&gt; 224

gccncagatc cagcgcccag agagacacca gagaaccac catggccccc tttgnagccc 60  
ctggcttctg gcatectgtt g ttgctgtgg ctgatagccc ccagcagggc ctgcacctgt 120  
gtcccacccc acccacagac ggccttctgc aattccgacc tcgtcatcag ggccaagtgc 180  
gtggggacac cagaagtcaa ccagaccacc ttataccagc gttatgagat caagatgacc 240  
aagatgtata aagggttcca agccttaggg gatgccgctg acatccggtt cgtctacacc 300  
cccgccatgg agagtgtctg cggatacttn cacagggtccc acaaccgnag cgaggagtgtt 360  
ctcattngct ggaaaactgt aggatggact tcttgacat tnactacctt gcagttttng 420  
tgggttcctt gggaacagtc tgaggtttag tttagcggtt ggggtt 466

&lt;210&gt; 225

&lt;211&gt; 782

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(782)

<223> tissue inhibitor of metalloproteinase 1  
(erythroid potentiating activity, collagenase  
inhibitor) (TIMP1) gene.

&lt;400&gt; 225

aggggcctta gcgtgccgca tcgccgagat ccagcgccca gagagacacc agagaacca 60  
ccatggcccc ctttgagccc ctggcttctg gcatectgtt gttgctgtgg ctgatagccc 120  
ccagcagggc ctgcacctgt gtcccacccc acccacagac ggccttctgc aattccgacc 180  
tcgtcatcag ggccaagtgc gtggggacac cagaagtcaa c cagaccacc ttataccagc 240  
gttatgagat caagatgacc aagatgtata aagggttcca agccttaggg gatgccgctg 300  
acatccggtt cgtctacacc cccgccatgg agagtgtctg cggatacttc cacagggtccc 360  
acaaccgcag cgaggagtgt ctcattgctg gaaaactgca ggatggactc ttgcacatca 420  
ctacctgcag tttcgtggct ccctggaaca ccctgagctt agctcagcgc cggggcttca 480  
ccaagacctt cactgttggc tgtgaggaat gcacagtgtt tccctgttta tccatcccct 540  
gcaaactgca gagtggcact cattgcttgt ggacggacca gctcctccaa ggctctgaaa 600  
agggcttcca gtcccgtcac cttgcctgcc tgcctcgga gccagggtgt tgcacctggc 6 60  
agtccctgcg gtcccagata gcctgaatcc tgcccgaggt ggaactgaag cctgcacagt 720  
gtccaccctg ttcccactcc catctttctt ccggacaatg aaataaagag ttaccacca 780

gc

782

<210> 226  
 <211> 353  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(353)  
 <223> 5' terminal sequence. ephrin -a1 (EFNA1)  
 gene.

<400> 226  
 acagctacta ctacatctca gccaaaccca tccaccagca tgaagaccgc tgcttgaggt 60  
 tgaaggtgac tgtcagtggc aaaatcactc acagtcctca ggcccatgtc aatccacagg 120  
 agaagagact tgcagcagat gaccagagg tgccgggttct acatagcatc ggtcacagtg 180  
 ctgccccacg cctcttccca cttgcctgga ctgtgctgct ccttccactt ctgctgctgc 240  
 aaaccccggtg aaggtgtatg ccacacctgg ccttaaagag ggaca ggctg aagagaggga 300  
 caggcactcc aaacctgtct tgggggccac ttccagagcc cccagccctt ggg 353

<210> 227  
 <211> 1480  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(1480)  
 <223> ephrin-a1 (EFNA1) gene.

<400> 227  
 gcggagaaag ccagtgggaa cccagaccca taggagaccc ggcgtcccg ctcggcctggc 60  
 caggcccccgc gctatggagt tcctctgggc ccctctcttg ggtctgtgct gcagtctggc 120  
 cgctgctgat cgccacacgg tcttctggaa cagttcaaat cccaagttcc ggaatgagga 180  
 ctacaccata catgtgcagc tgaatgacta cgtggacatc atctgtccgc actatgaaga 240  
 tcaactctgtg gcagacgctg ccatggagca gtacatactg tacctggtgg agcatgagga 300  
 gtaccagctg tgccagcccc agtccaagga ccaagtcgcg tggcagtgc accggcccag 360  
 tgccaagcat ggcccggaga agctgtctga gaagttccag cgcttcacac ctttcaccct 420  
 gggcaaggag ttcaaagaag gacacagcta ctactacatc tccaaaccca tccaccagca 480  
 tgaagaccgc tgcttgaggt tgaaggtgac tgtcagtggc aaaatcactc acagtcctca 540  
 ggcccatgtc aatccacagg agaagagact tgcagcagat gaccagagg tgccgggttct 600  
 acatagcatc ggtcacagtg ctgccccg cctcttccca cttgcctgga ctgtgctgct 660  
 ccttccactt ctgctgctgc aaaccccggtg aaggtgtatg ccacacctgg ccttaaagag 720  
 ggacaggctg aagagaggga caggcactcc aaacctgtct tggggccact ttccagagccc 780  
 ccagccctgg gaaccactcc caccacaggc ataagctatc acctagcagc ctcaaaacgg 840  
 gtcagtatta aggttttcaa ccggaaggag gccaaaccagc ccgacagtgc catccccacc 900  
 ttcacctcgg agggacggag aaagaagtgg agacagtcct ttcccaccat tctgccttt 960  
 aagccaaaga aacaagctgt gcaggcatgg tcccttaagg cacagtggga gctgagctgg 1020  
 aagggggccac gtggatgggc aaagcttgct aaagatgccc cctccag gag agagccagga 1080  
 tgcccagatg aactgactga aggaaaagca agaaacagtt tcttgcttgg aagccaggta 1140  
 caggagaggc agcatgcttg ggctgaccca gcatctccca gcaagacctc atctgtggag 1200  
 ctgccacaga gaagtttgta gccaggctact gcattctctc ccatcctggg gcagcactcc 1260

149/292

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ccagagctgt gccagcaggg g ggctgtgcc aacctgttct tagagtgtag ctgtaagggc 1320
agtgtccatg tgtacattct gcctagagt tagcctaaag ggcagggccc acgtgtatag 1380
tatctgtata taagttgctg tgtgtctgtc ctgatttcta caactggagt ttttttatac 1440
aatgttcttt gtctcaaat aaagcaatgt gttttttcgg 1480

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&lt;210&gt; 228

&lt;211&gt; 170

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(170)

<223> 3' terminal sequence. endothelin receptor  
type a (EDNRA) gene.

&lt;400&gt; 228

```

ttttaagggt tctgtaaact tttattttac acttatgggc cactgcaact cagggccttg 60
gcttctggct catttctaca aagttacttg ttgaaaagat gtagtaaagg tagaaattgg 120
aaatattcct gctagtaaac cacagttact taccagtcca taaataaaat 170

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&lt;210&gt; 229

&lt;211&gt; 4105

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4105)

&lt;223&gt; endothelin receptor type a (EDNRA) gene.

&lt;400&gt; 229

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gaattcgcg g cgcctcttg cgggtcccaga gtggagtgga aggtctggag ctttgggagg 60
agacggggag gacagactg g aggcgtgttc ctccggagtt ttctttttcg tgcgagccct 120
cgcgcgcgcg tacagtcac cgcgtgttct gacgattgtg gagaggcggt ggagaggcct 180
catccatccc acccggtcgt cgccggggat tggggtccca gcgacacctc cccgggagaa 240
gcagtgccca ggaagttttc tgaagccggg gaagctgtgc agccgaagcc gccgccgcgc 300
cggagcccg gacaccggcc accctccgcg ccaccacccc tcgctttctc cggcttctc 360
tggcccaggc gccgcgcgga cccggcagct gtctgcgcac gccgagctcc acggtgaaaa 420
aaaaagtga ggtgtaaaag cagcacaagt gcaataagag atatttcctc aaatttgcct 480
caagatgaa accctttgcc tcagggcac cttttggct g gcactggttg gatgtgtaat 540
cagtataat cctgagagat acagcacaat totaagcaat catgtggatg atttaccac 600
ttttcgtggc acagagctca gcttctctgt taccactcat caaccacta atttggctct 660
accagcaat ggtcaatgc acaactattg ccacagcag actaaaatta cttcagcttt 720
caatacatt aacactg tga tatctgtac tattttcatc gtgggaatgg tggggaatgc 780
aactctgtc aggatcatt accagaacaa atgtatgagg aatggcccca acgcgtgat 840
agccagtctt gcccttgagg acqtatctc tgtggtcatt gatctcccta tcaatgtatt 900
taagctgctg gctgggcgct ggccttttga tcacaatgac tttggcgat ttctttgca a 960
gtgtttcccc tttttgcaga agtcctcggt ggggatcacc gtcctcaacc tctgcgtct 1020
tagtggtgac aggtacagag cagttgcctc ctggagtcgt gttcagggaa ttgggattcc 1080
tttgtaact gccattgaaa ttgtctccat ctggatcctg tcctttatcc tggccattcc 1140
tgaagcgatt ggcttcgtca tggtagcctt tgaa tatagg ggtgaacagc ataaaacctg 1200
tatgtcfaat gccacatcaa aattcatgga gttctaccaa gatgtaaagg actggtggct 1260

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cttcgggttc tattttgtga tgcccttggt gtgcactgcg atcttctaca cctcatgac 1320
ttgtgagatg ttgaacagaa ggaatggcag cttgagaatt gccctcagtg aacatcttaa 1380
gcagcgtoga gaagtggcaa aaacagtttt ctgcttggtt gtaatttttg ctctttgctg 1440
gttccctctt cacttaagcc gtatattgaa gaaaactgtg tataacgaaa tggacaagaa 1500
ccgatgtgaa ttacttagtt tcttactgct catggattac atcgggtatta acttggaac 1560
catgaattca tgtataaacc ccatagctct gtattttgtg agcaagaa at ttaaaaattg 1620
tttcagtcga tgcctctgct gctgctgtta ccagtcctaaa agtctgatga cctcgggtccc 1680
catgaacgga acaagcatcc agtggaagaa ccacgatcaa aacaaccaca acacagaccg 1740
gagcagccat aaggacagca tgaactgacc acccttagaa gcactcctcg gtactcccat 1800
aatcctctcg gagaaaaaaa tc acaaggca actgtgactc cggaatctc ttctctgatc 1860
cttcttctct aattcactcc cacaccaag aagaaatgct ttccaaaacc gcaaggtaga 1920
ctggtttatc caccacaac atctacgaat cgtacttctt taattgatct aatttacata 1980
ttctgcgtgt tgaattcagc actaaaaaat ggtgggagct gggggagaat gaagactgtt 2 040
aaatgaaacc agaaggatat ttactacttt tgcattgaaa tagagcttc aagtacatgg 2100
ctagctttta tggcagttct ggtgaatggt caatgggaac tggtcacat gaaactttag 2160
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aatagtatc aggtgagcaa ttagattagt attttccacg tcaactattta tttttttaa 2400
acacaaatc taaagctaca acaataacta caggccctta aagcacagtc tgatgacaca 2460
tttggcagtt taatagatgt tactcaaaga attttttaag aactgtattt tttttttaa 2520
atggtgtttt attacaagg accttgaaca tgttttgtat gttaaattca aaagtaatgc 2580
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tcagtgcact gtatatagaa gtctaaaaca cacctaagag aaaaagatcg aatttttcag 2760
atgattcggg aattttcatt caggatattg taatagtgc atatatatgt atatacatat 2820
cacctcctat tctcttaatt ttgttaaaa tgttaactgg cagtaagtct tttttgatca 2880
ttcccttttc catataggaa acat aatttt gaagtggcca gatgagtta tcatgtcagt 2940
gaaaaataat taccacaaa tgccaccagt aacttaacga ttcttactt cttggggttt 3000
tcagtatgaa ctaactccc caccacaaca tctccctccc acattgtcac catttcaaag 3060
ggcccacagt gacttttget gggcattttc ccagatgttt acagactgtg agtacagcag 312 0
aaaatctttt actagtgtgt gtgtgtatat atataaaca ttgtaaattt cttttagccc 3180
atttttctag actgtctctg tggaatatat ttgtgtgtgt gatatatgca tgtgtgtgat 3240
ggtatgtatg gatttaattc aatctaataa ttgtgccccg cagttgtgcc aaagtgcata 3300
gtctgagcta aaatctaggt gattgttcat catgacaa cc tgcctcagtc cattttaacc 3360
tgtagcaacc ttctgcattc ataaatcttg taatcatgtt accattacaa atgggatata 3420
agaggcagcg tgaagcaga tgagctgtgg actagcaata tagggttttg tttgggttgt 3480
tggtttgata aagcagttat tggggtcata ttgtttcctg tgctggagca aaagtcatta 3540
cactttgaag tattatattg ttcttactc caattcaatg tggatgatga attgccaggt 3600
tgtctgatat ttctttcaga cttcgccaga cagattgtcg ataataaatt aggtgaagata 3660
atttgttggg ccatatttta ggacaggtaa aataacatca ggttcagtt gcttgaattg 3720
caaggctaag aagtactgcc cttttgtgtg ttagcagtc aatctattat t cactggcg 3780
catcatatgc agtgatatat gcctataata taagccatag gttcacacca tttgttttag 3840
acaattgtct tttttcaag atgctttgtt tctttcatat gaaaaaaatg cattttataa 3900
attcagaaag tcatagattt ctgaaggcgt caacgtgcat tttatttatg gactggtaag 3960
taactgtggt ttactagcag gaatat ttcc aattttctacc ttactacat cttttcaaca 4020
agtaactttg tagaaatgag ccagaagcca aggcctgag ttggcagtg ccataagtg 4080
taaaataaaa gtttacagaa acctt 4105

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&lt;210&gt; 230

&lt;211&gt; 240

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(240)

<223> 3' terminal sequence. growth factor  
receptor-bound protein 2 (GRB2) gene.

<400> 230

ggtttcttgt tttttattat tggcgtcagt agngactata cgtggcctta aacgtcatgc 60  
actgatggac agaagagaaa aaaggatgaa aaaaaagaca aaggagggga aagaggagca 120  
gcagtgaan tttgtaataa aaactcttct taatttatag gtaagttttg gcatttttaa 180  
atccaacgcc cctcccacc ccctaaagtt ccaaccaaag tgagagggtc acagggtgac 240

<210> 231

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(475)

<223> 5' terminal sequence. growth factor  
receptor-bound protein 2 (GRB2) gene.

<400> 231

cttaatggaa aagacgggctt cattcccaag aactacatag aaatga aacc acatccgtgg 60  
ttttttggca aaatccccag agccaaggca gaagaaatgc ttagcaaaca gcggcacgat 120  
ggggcctttc ttatccgaga gagtggagagc gctcctgggg acttctccct ctctgtcaag 180  
tttgaaaacg atgtgcagca cttcaagggtg ctccgagatg gagccgggaa gtacttcctc 240  
tgggtggtga agttcaattc ttgga atgag ctgggtggatt atcacagatc tacatctgtc 300  
tccagaaacc agcagatatt cctgcgggga cattaggaac aggtgccaca gcaggccgac 360  
atacgttoca ggggcctttt ttgattttt gattccccag gggggnttgg ngagggtggg 420  
ttttccgccg ggggagattt tattccatgt tcntgggttn aatttaggaa ccntt 475

<210> 232

<211> 1109

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(1109)

<223> growth factor receptor-bound protein 2  
(GRB2) gene.

<400> 232

gccagtgaat tcgggggctc agccctcctc cctcccttcc ccctgcttca ggtgctgag 60  
cactgagcag cgctcagaat ggaagccatc gccaaatatg acttcaaagc tactgcagac 120  
gacgagctga gttcaaaaag gggggacatc ctcaagggtt tgaacgaaga atgtgatcag 180  
aactggtaca aggcagagct taatggaaaa gacggcttca ttccaagaa ctacatagaa 2 40  
atgaaaccac atcctgtggt ttttgcaaa atccccagag ccaaggcaga agaaatgctt 300  
agcaaacagc ggcacgatgg ggcctttctt atccgagaga gtgagagcgc tcctggggac 360  
ttctccctct ctgtcaagtt tggaaacgat gtgcagcact tcaagggtgct ccgagatgga 420  
gccgggaagt acttctctg ggtggtgaag ttcaattctt tgaatgagct ggtggattat 480  
cacagatcta catctgtctc cagaaaccag cagatatctc tgcgggacat agaacagggtg 540  
ccacagcagc cgacatacgt ccaggccctc tttgactttg atccccagga ggatggagag 600  
ctgggcttcc gccggggaga ttttatccat gtcatggata actcagaccc caactggtgg 660



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aaaggagctt gccacggg ca gaccggcatg tttccccgca attatgtcac ccccgatgaac 720
cggaacgtct aagagtcaag aagcaattat ttaaagaaag tgaaaaatgt aaaacacata 780
caaaagaatt aaaccacaa gctgcctctg acagcagcct gtgagggagt gcagaacacc 840
tggccgggtc accctgtgac cctctcactt tggttggaac tttagggggg gggagggggc 900
gttgatttta aaaaagccaa aacttaccta taaattaaga agagttttta ttacaaattt 960
tcaactgtgc tcctctttcc cctcctttgt cttttttttc atcctttttt ctcttctgtc 1020
catcagtgc tgacgtttta ggccacgtat agtcctagct gacgccaata ataaaaaaca 1080
agaaaccaa aaaaaaaac ccgaattca 1109
```

&lt;210&gt; 233

&lt;211&gt; 446

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(446)

<223> 3' terminal sequence. jun d proto -oncogene  
(JUND) gene.

&lt;400&gt; 233

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cgcgctctc ggctgccnng ntgtacaccg cgccgaaag tggggctccg agggggcgca 60
ctcaaaaccc tgcctttcct ttacttttac tttttttttt tttctttgg aagagagaag 120
aacagagtgt tcgattctgc cctatttatg tttctactcg ggaacaaacg ttggttgtgt 180
gtgtgtgtgt tttcttgtgt tggtttttta a agaaatggg aagaagaaaa aaaaattctc 240
cgcccccttc ctcgatctcg ctccccctt cggttctttc gaccgggtcc cccctccctt 300
tttttgttct gttttgtttt gttttgctac gagtcacat tcctgtttgt aatccttggg 360
ttcgnccggt tttctgtttt cagtaaagtc tcgttacggc aaaacctcgt gccgaatttt 420
tggggctcga ggggcaaat ttccca 446
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&lt;210&gt; 234

&lt;211&gt; 1891

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1891)

&lt;223&gt; jun d proto -oncogene (JUND) gene.

&lt;400&gt; 234

```
ccgaggttat aagaggggcg acaagtggcg cgccgcagga gccgccgcca gtggagggcc 60
gggcgctgcg gccgcggccg gggcgggcg agggccgagc ggacgggggg gcgcggggcc 120
cccgaggagc cgcgccact ccccccggg ccggcgcggc gggggaggcg gaggatggaa 180
acaccttct acggcgatga ggcgctg agc ggcctggcg gcgcgccag tggcagcggc 240
ggcacgttcg cgtccccggg ccgcttggtc ccggggcgcg ccccgacggc cgcggccggc 300
agcatgatga agaaggacgc gctgacgctg agcctgagt agcaggtggc ggcagcgctc 360
aagcctgcgc ccgcgccgc ctctacccc cctgcgcgc acggcgcccc cagcgcgga 420
cccccgagc gctgctgc ctctcccgac ctggggctgc tgaagctggc ctccccgag 480
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ttcctctacc ccaagtggtg gccagcgag gacagaggt tcgccagggg cttcgtcaag 600
gccctggagg atttacacaa gcagaaccag ctggcgcgcg gccgggc cgc tgcgcggcc 660
gccgccgccc ccggggggcc ctcgggcagc gccacgggct ccgcgcccc cggcgagctg 720
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ggcgccgggg gcgcgggggg cgccgcgacg gtcgccttcg ctgccgaacc tgtgcccttc 840
ccgcccggcg cacccccagg cgcgt tgggg ccgcccgcgcc tggctgcgct caaggacgag 900
ccacagacgg tgcccagcgt gccgagcttc ggcgagagcc cgccgttgct gcccatcgac 960
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cagctcaagc agaaagtcct cagccacgct aacagcggct gccagctgct gcccagcac 1200
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gttcgattct gccctattta tgtttctact cggggaacaa acgttggttg tgtgtgtgtg 1680
tgttttcttg tgttggttt ttaaagaaat aaaaaaatt ctcc gccct 1740
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tgttttgttt tgttttcta cgagtccaca ttctgtttg taatccttg ttcgcccgt 1860
tttctgtttt cagtaaagtc tcgttacgcc a 1891
```

&lt;210&gt; 235

&lt;211&gt; 421

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(421)

<223> 3' terminal sequence. swi/snf related,  
matrix associated, actin dependent regulator of  
chromatin, subfamily a, member 2 (SMARCA2) gene.

&lt;400&gt; 235

```
acaaaaagtc ttcaagccac gagcggaggg cattcctgca ggccatcttg gagcatgagg 60
aggaaaatga ggaagaagat gaagtaccgg acgatgagac tctgaaccaa atgattgctc 120
gacgagaaga agaatttgac ctttttatgc ggatggacat ggaccggcgg agggaagatg 180
cccggaaacc gaaacggaag ccccgtttaa tggaggagga tgagctgcc tctggntca 240
ttaaggatga cgtgaagta gaaaggctca cctgtgaaga agaggaggag aaaatatttg 300
ggagggggtc ccgcagcgc cgtgacgtgg actacagtga cgccctcac gagaagcagt 360
ggctaaaggg cntcgaaga cggcatttng gaggaattng aagaggaata c ggtaagaa 420
g 421
```

&lt;210&gt; 236

&lt;211&gt; 438

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(438)

<223> 5' terminal sequence. swi/snf related,  
matrix associated, actin dependent regulator of

chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 236

```

tgccaatttt ctgccgggca ctcttaaaca ctgactgtaa gacgatggag tcttcataga 60
tctgggatcc ctccagggtg aacgtctgag cg ttgtgaca gagaagcatg acatccttct 120
ccaggctgcc taggctccgg tacttatgat tacgaatcct ttcctttatt tttttgaaat 180
ccactggctt cctaattaat tcatagtatt ctggtaattc tttccttgaa ggtaactgaa 240
tgaagacttc actgagctgt cgccctgaac tgtttccttc tatttccaac tgagaattac 300
tgggcacctt ctccacgtta caccatctct tgtagtttat cacagtattc gatgattagc 360
gttcatctgg ctttgtcagt ttggggggga tttggtgaca gntttntcag cgggaggggc 420
gcctcttctc ttcttagg                                     438

```

<210> 237

<211> 5257

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(5257)

<223> swi/snf related, matrix associated, actin  
dependent regulator of chromatin, subfamily a,  
member 2 (SMARCA2) gene.

<400> 237

```

aaaaattttc tgttacaaa ttttacaact tctaataaga ctactataac tttatgtaa 60
ctgatgaaga tgtgctgatt aacatattct gtgatatggt ttacaacttt taatcataat 120
tgtccatgat tttggaatgc tgttatttat cagtaaatgt aaaatatgtg aggcatttag 180
ccatacacac actagaactt tttaaaactt tgctctatag tgtaatta ta aactgatgac 240
tattatcttc atacattgag tcttcatgca tcaatgaaat gaaaaatata ggagtagatg 300
tccacgcccc cagaccctgg tgcgatgcc caccagggc cttcgccggg gcctgggcct 360
tcccctgggc caattcttgg gcctagtcca ggaccaggac catccccagg ttccgtccac 420
agcatgatgg ggccaagtcc tggacc tcca agtgtctccc atcctatgcc gacgatgggg 480
tccacagact tccacagga aggcattgat caaatgcata agcccatcga tggatatacat 540
gacaagggga ttgtagaaga catccattgt ggatccatga agggcactgg tatgcgacca 600
cctcacccag gcatggggcc tcccagagt ccaatggatc aacacagcca aggttatatg 660
tcaccacacc catctccatt aggagcccca gagcacgtct ccagccctat gtctggagga 720
ggcccaactc cacctcagat gccaccaagc cagccggggg ccctcatccc aggtgatccg 780
caggccatga gccagcccaa cagaggtccc tcacctttca gtctgtcca gctgcatcag 840
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ctgcagcttg cagtccaggg gaaaaggacg ttgcctggct tgcagcaaca acagcagcag 960
caacagcagc agcagcagca gcagcagcag cagcagcagc agcaacagca gccgcagcag 1020
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agaatgcggc gactgatggc tgaagatgag gagagttata gaaaactgat tgatcaaaag 1860
aaagacaggc gtttagctta ccttttgac cagaccgatg agtatgtagc caatctgacc 1920

```

aatctggttt gggagcacia gcaagcccag gcagccaaag agaagaagaa gaggaggagg 1980  
aggaagaaga aggtctgagga gaatgcagag ggtggggagt ctgccctggg accggatgga 2040  
gagcccatag atgagagcag ccagatgagt gacctccctg tcaaagtac tcacacagaa 2100  
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caagccaagg ggtccttct cacaga tggg tctgagaaag ataagaagg gaaaggagg 3300  
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cgcatcgggc agcagaacga ggtccgggta ctgaggctct gtaccgtgaa cagcgtggag 3840  
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cgaggaaaag ccaaacctgt agtgagcgat tttgacagcg atgaggagca ggatgaacgt 4980  
gaacagtcag aaggaa gtgg gacggatgat gagtgatcag tatggacct tttccttgg 5040  
agaactgaat tccttccctc cctgtctcat ttctaccag tgagttcatt tgtcatatag 5100  
gcactgggtt gtttctatat catcatcgtc tataaactag ctttaggata gtgccagaca 5160  
aacatatgat atcatggtgt aaaaaacaca cacatacaca aatatttgtg accaa atggg 5220  
cctcaaagat tcagattgaa acaaacaaaa agctttt 5257

&lt;210&gt; 238

&lt;211&gt; 507

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(507)

<223> 3' terminal sequence. protein phosphatase 2  
(formerly 2a), regulatory subunit b (pr 52), gamma  
isoform (PPP2R2C) gene.

<400> 238

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tacatgctca cccgggacta ccttacagtc tatggatggg acctgaacat ggaggcaaga 60
cccatagaga cctaccaggt ccatgactac ctctggagca agctctgttc cctgtacgag 120
aacgactgca ttttcgacaa gtttgaatgt gcctggaacg ggagcgacan tncatcatga 180
ccggggccta caacaacttc ttccgcatgt tcgatcgga caccaagcgg gacgtgacct 240
tgggaggcct cgagggaag cagcaagccc cgggctgtgc tcaagccacg gcgcgtgtgc 300
gtgggggggc aagcgccggc gtgnatga ca tcagtgtggg acagcttggg acttcaccaa 360
gaagatcctg cacacggcct ggcacccggc tgaggaacat catttgccat tcgccgccac 420
caacaacctg ttacatcttt ccaggggcaa ggtaaatttt tgacattgca ttaggtattn 480
tgcaatttcc cggnccttgc caacca 507
```

<210> 239

<211> 521

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(521)

<223> 5' terminal sequence. protein phosphatase 2  
(formerly 2a), regulatory subunit b (pr 52), gamma a  
isoform (PPP2R2C) gene.

<400> 239

```
taaacagaca attactgcc aacacaattc tggcctagga aagcggggnn gggagggggc 60
ccaaacttcc tgtgtccaca cactgccacc tctgcagctg tcctcatcag tgggtgtgact 120
ttcttccct ccttgcatg cggtcgtgaa ggcatgtcg gggatgactt gcatgaggct 180
gggtggcagg ggccgggaac tgcacatacc tagtgcattg cagagtttac cttgtcctgg 240
aagatgtaca ggttgttggg ggcggcgatg gcaatgatgt tctcagccgg gtgccaggcc 300
gtgtgcagga tcttcttggg gaagtccaag ctgttccaaa atgatgtcat cagccgggcc 360
cttgccccc acgnaaangg nccnttggtt tnagcaaagc ccng ggtttg ttgcttttcc 420
ctngnaggcn tncaggntca agtnccnttt ggtnttncce gatcgaacat ncggaagaat 480
tttttttagg ccccntcat gatgaacgtg tncgttccct t 521
```

<210> 240

<211> 350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(350)

<223> 3' terminal sequence. thrombospondin 3  
(THBS3) gene.

<400> 240

```
cagattcatt nnnngganntg cctgtgacaa ttgccccaac gttcccaaca atgaccagaa 60
ggacacagat ggcaatgggg aaggagatgc ctgtgacaac gac gtggatg gggatgggtgc 120
aggcctgggg ctgaaggggt ggctggggga cctgtgagaa tttggatcag gtggggatga 180
agcagggaag ctaggaagtc tctgtgaaat agggaggcag gcttntggac gttggcctgg 240
gtgaggagag attacctgca gcagatgtca ataggaatnt gaggtagggc gtagtnttag 300
gcagagtttg gactagaggg t nagacaaga aacaggcaga tttcctggcc 350
```

<210> 241

<211> 2871

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2871)

<223> thrombospondin 3 (THBS3) gene.

<400> 241

```
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gccagtcagg atctgcaggt aattgacctg ctgactgtgg gcgagtctcg gcagatggta 120
gctgtggcag agaagatccg gacagccttg ctcactgctg gggacatcta cctcttatcc 180
accttccgcc tgccccccaa gcagggtggg gtccctcttg g cctctatcc tcgccaagac 240
aacactcgat ggctggaggc ctctgtttga ggcaagatca acaaagtact ggtgcgatac 300
cagcggggagg atggcaaaagt ccacgccgtg aacctacagc aagcgggcoct ggctgatggg 360
cgcacacaca cagttctcct gcgactccga ggtccctcca gaccagccc tgccctacat 420
ctctacgtgg actgcaaaact gggtgacca catgcaggcc ttccagcact ggccccatt 480
cctccagcgg aggtcgatgg gctggagatt aggactggac agaaggcgta tttgaggatg 540
cagggcctttg tggaaatctat gaaaattatt ctgggtgggt ccatggcccg ggtaggagcc 600
ctgagtgaat gtccattcca aggggacgag tccatccaca gtgcagtga caatgcactg 6 60
cactccattc taggggagca gaccaaggcg ctggtcacc aactcaccct cttcaaccag 720
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aacaccatta tggagtgtca ggtgtgcggc ttccatgagc agcgttccca ctgcagcccc 840
aatccctgct tccgaggtgt ggactgcatg gaagtgtacg agtaccagag ctaccgctgt 900
gggcccctgcc cccctggcct gcagggcaac ggcacccact gcagtgcacat caatgagtgt 960
gctcacgctg acccctgttt ccggggctcc agctgcatca acaccatgcc cggcttccac 1020
tgtgaggcct gtccctcgagg gtacaagggc acacagggtg ctggtgtggg cattgactat 1080
gcccggggcca gcaaac aggt ctgcaatgac atcgatgaat gcaacgatgg caacaatggt 1140
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cgccctgggtt tcctgggcaa ccagagccag ggctgcctcc cagcccggac ctgccacagc 1260
ccagcccaca gcccctgcca catccatgct cactgtctct ttgaacgcaa tgggtg cagtg 1320
tcctgccagt gtaacgtggg ctgggctggg aatgggaacg tgtgtgggac tgacacagac 1380
atcgatggct acccagacca agcactgccc tgcatggaca acaacaaaca ctgcaaacag 1440
gacaactgcc ttttgacacc caactctggg caggaagatg ctgataatga tgggtgtggg 1500
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ctgtgtccca acaagacca gcaaaactca gatacagatt catttgggtg tgccctgtgac 1620
aattgcccc aagttcccaa caatgaccag aaggacacag atggcaatgg ggaaggagat 1680
gcctgtgaca acgacgtgga tggggatggc atccccaatg gattggacaa ttgccctaaa 1740
gtccccaacc cactacagac agacagggat gaggacgggg tgggagatgc ttgcgacagc 1800
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tgtgatacta atgaagacag cgatggggat gggcatcagg acaccaagga caactgcccc 1920
cagctgccaa atagctccca gctggactct gataacgatg gac ttggaga tgagtgtgat 1980
gggatgatg acaatgatgg catccagat tatgtgcctc ctggtcccca taactgccgc 2040
```

158/292

```

ctggtaccca atcccaatca gaaggactca gatggcaatg gcgttggtga tgtgtgtgag 2100
gatgactttg acaatgatgc tgtggtcgac cccctggatg tgtgtcctga aagtgcagag 2160
gtaacgctta cggatttt cg gccctatcag accgtcgtcc tggatcctga gggatgatgct 2220
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agtgaccctg gcttggcagt tggatacacg gccttcaatg gtgtggactt tgaaggcacc 2340
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gtggcgggatt ctggggtgat cattgacaca tccatgcgag gggggcgtct tgggtgtattc 2760
tgcttctccc aagaaaacat aatttggtcc aatctccagt atcgatgcaa tgacacagt 2820
cctgaggact ttgagccatt ccggaggcag ctgctccagg gaagggtgtg a 2871

```

&lt;210&gt; 242

&lt;211&gt; 509

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(509)

<223> 3' terminal sequence. actin, gamma 1 (ACTG1)  
gene.

&lt;400&gt; 242

```

cacttttatt ttnccttaca caatgacgtg ttgctggggc ctaatgttct cacataacag 60
tagaaaacca aaatttggtg tcatctcttc aaagantcga ganttgcgta caaaaaaac 120
cttacataan ttaagantga ntacatttac aggcgtaaat gcaaaccgnt tccaactcaa 180
agcaagtaac agcccacggt gttctggcca aagacatcag ctaagaaagg aaactggggn 240
cctacggctt gggactttcc aaccctggac aggaccgca agncaaac aactgggttc 300
ttgccagcct ctaggaggaa ttcccggaac actcaggccc tggacangtt taataccagg 360
ggggancagt taactttcan tacaggggnc aaaatcaggc aacagttt tt accantccag 420
tggtggttt cnggttacag gtttcagggg cattttnttt tcggaggggt tnttccggt 480
tcgtgagggt aggtgagggt tttntgctt 509

```

&lt;210&gt; 243

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(393)

<223> 5' terminal sequence. actin, gamma 1 (ACTG1)  
gene.

&lt;400&gt; 243

```

gatcacgcc ctggccccag caccatgaag atcaagatca tcgcaccccc agagcgcaag 60
tactcgggtg ggatcgggtg ctccatcctg gcctcactgt ccaccttc a gcagatgtgg 120
attagcaagc aggagtacga cgagtcgggc ccctccatcg tccaccgcaa atgtttctaa 180
acggactcag cagatgcgta gattttgctg catgggttaa ttgagaatag aaatttgccc 240

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ctgggaaatt gcacacacct catgctagcc tcacgaaact gggaataagc ctttcgaaaa 300  
gaaattgtcc ttgaagcttg tatctgg tat cagcactggg ntgttaggaa nttgttgctg 360  
atttttgacc ttgtanttga agtttaactg ttt 393

&lt;210&gt; 244

&lt;211&gt; 1919

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1919)

&lt;223&gt; actin, gamma 1 (ACTG1) gene.

&lt;400&gt; 244

gtctcagtcg ccgctgccag ctctgcact ctgtttcttc gccgctccgc cgtcgcgttt 60  
ctctgccggt cgcaatggaa gaagagatcg ccgcgctggt cattgacaat ggctccggca 120  
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aacattagga cccagcaaca cgtcattgtg taaggaaaaa taaaagtgtc g ccgtaacc 1919

&lt;210&gt; 245

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer



<220>  
<221> misc\_feature  
<222> (1)..(467)  
<223> 3' terminal sequence. integrin, alpha 6  
(ITGA6) gene.

<400> 245  
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cacttncaac ttggacactc gggaggacaa cgtgatcccg aaatatggag accccgggag 120  
cctcttcggc ttctcgctgg ccatgcactg gcaactgcag cccgaggaca agcggtgtt 180  
gctcgtgggg gcccgcgcg agnaagcgct tccactgcag agagccaac a gaacgggagg 240  
gctgtacagc ttgcgacatc accgcccggg ggccatgcac ggggatcgag ttnataacg 300  
atgcttgacc ccacgtcaga aagcaaggaa gattagtgg atngggggtc aacgtccaga 360  
gccaaagttc agggggcaag gtogtgacat gtgttnaccc tattgaaaaa aggcagcgtt 420  
ttattacgna gcangatttc cgagaca ttt ttgggcgttt tttttcc 467

<210> 246  
<211> 473  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(473)  
<223> 5' terminal sequence. integrin, alpha 6  
(ITGA6) gene.

<400> 246  
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cacatgtcac gaccttgccc cctggacctt ggctctggac ggtgaccccc atccactgat 180  
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cccgggcggt ggatgtcgca gctgtacagc cctcccgttc tgttggtct ctgcagtggg 300  
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gccagtgcac ggccacgca gaaagccgaa gaggttcccc ggggtnttcc atattttccg 420  
gatcaagttg ttcctnccga gttttccaag tttgaagggt tgcgcaaggc cgt 473

<210> 247  
<211> 5611  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(5611)  
<223> integrin, alpha 6 (ITGA6) gene.

<400> 247  
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ccgctcccct ccccggtgct ccgcccattg ccgcccgcgg gcagctgtgc ttgctctacc 180  
tgtcggcggg gctcctgtcc cg gctcggcg cagccttcaa cttggacact cgggaggaca 240  
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&lt;210&gt; 248

&lt;211&gt; 406

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(406)

<223> 3' terminal sequence. rad9 (s. pombe)  
homolog (RAD9) gene.

&lt;400&gt; 248

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aggatcctgn tcacagntca ccgcaggnc a gngncaggaa gcagccctgg gggantggaa 180
cgntgctatt gattcattaa aaaaagaaaa gaaaaa taca ccaaggttcc atnttccccg 240
tgacaggtgg gcctnagggg tcggggtnac cccccccag natggcagca tgattntnt 300
acaatcaatc catcatntgg gccacagggt ggttttcggg ggctattnt tggtttggc 360
gaaattncgg gntggggtaa tgggtnggcc tccagggtta aggcca 406
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&lt;210&gt; 249

&lt;211&gt; 2102

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2102)

&lt;223&gt; rad9 (s. pombe) homolog (RAD9) gene.

&lt;400&gt; 249

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at 2102
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&lt;210&gt; 250

&lt;211&gt; 365

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(365)

<223> 3' terminal sequence. activating  
transcription factor 3 (ATF3) gene.

&lt;400&gt; 250

tccaatattt attattctga caggtagga atactaggat aaataagtaa tatttntct 60

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```

tacagaaaat tgtaatgata ccattgagta caattaaaca ctctgagaat ttcacagaaa 120
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catctctcca ctgactgtgg ntttcaaccn caaggnaagg gaaatgggat attccttggg 360
ctctt                                     365

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&lt;210&gt; 251

&lt;211&gt; 453

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(453)

<223> 5' terminal sequence. activating  
transcription factor 3 (ATF3) gene.

&lt;400&gt; 251

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aagaaaacta ggcaatgtac tcttcgatg tttgtgtcac acaacactga tgtgactttt 180
atatgctttt tctcagatct ggtttctaag agttttggcg cgggcggggc tgtcaccacg 240
tgcagtatct caagatattc aggtgggcca gaagagcttg tcagcaagag ggaggacag 300
aattctccca ggcgtt aaca caaaatccat ggggcagtat ggatgggcag gtcntctgt 360
tggcaaactc agttcccaag tcacagggaa gganaggcag gaaagtttca actttcccaa 420
agggtttagg ggcttttcca cttcaatgtc tta                                     453

```

&lt;210&gt; 252

&lt;211&gt; 2056

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2056)

<223> activating transcription factor 3 (ATF3)  
gene.

&lt;400&gt; 252

```

gcagccaggc gcgcaactga cagctctctt ctctcgccgc cgcccagagc cacccttcag 60
cccgcgcgcc ggccgtgagt cctcggtgct cgcccgccgg ccagacaaac agcccgcccg 120
accctgtccc gacctggcc gccccgagcg gagcctggag caaaatgatg cttcaacacc 180
caggccaggt ctctgcctcg gaagtgagt cttctgccat cgtcccctgc ctgtcccctc 240
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ggtttgccat ccagaacaag cacctctgcc accggatgtc ctctgcgctg gaatcagtca 360
ctgtcagcga cagaccctc ggggtgtcca tcacaaaagc cgaggtagcc cctgaagaag 420
atgaaaaggaa aaagaggcga cgagaaagaa ataagattgc agctgcaaag tgccgaaaca 480
agaagaagga gaagacggag tgctgcagc tttag tatta gcagagccac agcccgctc 540
tgtggcatca ccagggtttc tctgaagaag agggctgtca ttttctaaa cccagtgtc 600
ctctcccatc tccatcttc ctctgcagc ttgatgagcc ccggtgtgtc ccaggagtcg 660
gagaagctgg aaagtgtgaa tgctgaactg aaggctcaga ttgaggagct caagaacgag 720
aagcagcatt tga tatacat gctcaacctt catcggccca cgtgtattgt ccgggctcag 780

```

165/292

```
aatgggagga ctccagaaga tgagagaaac ctctttatcc aacagataaa agaaggaaca 840
ttgcagagct aagcagtcgt ggtatggggg cgactgggga gtcctcattg aatcctcatt 900
ttatacccaa aaccctgaag ccattggaga gctgtcttcc tgtgtacctc tagaa tccca 960
gcagcagaga accatcaagg cgggagggcc tgcagtgatt cagcaggccc ttcccattct 1020
gccccagagt gggctcttga ccagggaag tgcatctttg cctcaactcc aggatttagg 1080
ccttaacaca ctggccatcc ttatgttcca gatggccccc agctggtgtc ctgcccgcct 1140
ttcatctgga ttctacaaaa aaccaggatg cccaccgtta gattcaggca gcagtgtctg 1200
tacctcgggt gggagggatg gggccatctc cttcaccgtg gctaccattg tcaactcgtag 1260
gggatgtgga gtgagaacag catttagtga agttgtgcaa cggccagggt tgtgctttct 1320
agcaaatacg ctgttatgtc cagaaattgt gtgtgcaaga aaactaggca atgtactctt 1380
ccgatgtttg tgtcacacaa cactgatgtg acttttatac gctttttctc agatctggtt 1440
tctaagagtt ttggggggcg gggctgtcac cacgtgcagt atctcaagat attcaggtgg 1500
ccagaagagc ttgtcagcaa gaggaggaac agaattctcc cagcgttaac acaaaatcca 1560
tgggcagcat gatggcaggc cctctgttgc aaactcagtt ccaa agtcac aggaagaaaag 1620
cagaaagtgc aacttccaaa gggtaggac tctccactca atgtcttagg tcaggagttg 1680
tgtctaggct ggaagagcca aagaaatatt ccattttcct ttcttgtggt ttgaaaccac 1740
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attggatgtc aaaagcattt tttttgtcat gtagctgttt taagaaatct ggcccagggt 1860
gtttgcagct gtgagaagtc actcacactg gccacaagga cgctggctac tgtctattaa 1920
aattctgatg tttctgtgaa attctcagag tgtttaattg tactcaatgg tatcattaca 1980
atttctgta agagaaaata ttacttattt atcctagtat tctaacctg tcagaata at 2040
aatattgtg gtaaaa                                     2056
```

&lt;210&gt; 253

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(502)

<223> 3' terminal sequence. v-akt murine thymoma  
viral oncogene homolog 2 (AKT2) gene.

&lt;400&gt; 253

```
acatcatctc gtacatgacc acaccagacc cantacnntt tccacggccc ggccatagtc 60
attgtcctcc agcacctcag gcgccaggta ctccggggtc ccacagaagg ttttcatggt 120
ggcccgcgtc ctgatgccct ctttgcaag gccaaagtca gtgatcttga tgtggccatc 180
tttgtccagc atgaggtttt ccagcttgat gtgcgggtat accacgtccc gcgagtcaa 240
gtactcaaga gccagacaa tctctgcacc ataaaaccgg gcccgctcct ctgtgaagac 300
acgctcccgg ggacagggtg gaagaacagc tcacccccgt tgggcatact ccattcaca 360
aggcacaggg cgggtcgtgg ggtctgggaa gggcattant ttcaggcggc agttgaggga 420
acggggttgc nggggtgttt ctgggaggga cccggttttt cggttgattn ttttgaggcg 480
atttcatcc nttgggcaat tt                                     502
```

&lt;210&gt; 254

&lt;211&gt; 1715

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1715)

<223> v-akt murine thymoma viral oncogene homolog  
2 (AKT2) gene.

<400> 254

```
gaattccagc ggcgcgccg ttgccgctgc cgggaaacac aaggaaagg aaccagcgc a 60
gcgtggcgat gggcggggt agagccccgc cggagaggct gggcggtgc cggtagacaga 120
ctgtgccctg tccacggtgc ctctgcatg tcctgctgcc ctgagctgtc ccgagctagg 180
tgacagcgta ccacgctgcc accatgaatg aggtgtctgt catcaaagaa ggctggctcc 240
acaagcgtgg tgaatacatc aagacctgga ggccacgg ta ctctctgctg aagagcgacg 300
gctccttcat tgggtacaag gagaggcccg agggccctga tcagactcta ccccccttaa 360
acaacttctc cgtagcagaa tgccagctga tgaagaccga gaggccgcga cccaacacct 420
ttgtcatacg ctgctgcag tggaccacag tcatcgagag gaccttcac gtggattctc 480
cagacgagag ggagga gtgg atgcgggcca tccagatggg cgccaacagc ctcaagcagc 540
gggccccagg cgaggacccc atggactaca agtgtggctc cccagtgac tcctccacga 600
ctgaggagat ggaagtggcg gtcagcaagg caggggctaa agtgaccatg aatgacttcg 660
actatctcaa actccttggc aagggaaacct ttggcaaagt catcctggtg cgggagaa gg 720
ccactggccg ctactacgcc atgaagatcc tgcgaaagga agtcatcatt gccaaaggatg 780
aagtgcctca cacagtcacc gagagccggg tcctccagaa caccaggcac ccgttctca 840
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acgggggtga gctgttcttc cacctgtccc gggagc gtgt cttcacagag gagcgggccc 960
ggttttatgg tgacagatt gtctcggtc ttgagtactt gactcgcg gacgtggtat 1020
accgcgacat caagctggaa aacctcatgc tggacaaaga tggccacatc aagatcactg 1080
actttggcct ctgcaaagag ggcacagtg acggggccac catgaaaacc ttctgtggga 1140
ccccggagta cctggcgctt gaggtgctgg aggacaatga ctatggccgg gccgtggact 1200
ggtgggggct ggtgtggtc atgtacgaga tgatgtgcgg ccgcctgccc ttctacaacc 1260
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tcagccccga ggccaagtcc ctgcttgcgt ggctgcttaa gaaggacccc aagcagaggc 1380
ttggtggggg gccagcgat gccaaggagg tcatggagca caggttcttc ctacagcatca 1440
actggcagga cgtggtccag aagaagctcc tggcaccctt caaacctcag gtcagtcgcg 1500
aggtcgacac aaggtacttc gatgatgaat ttaccgccc gtccatcaca atcacacccc 1560
ctgaccgcta tgacagcctg ggctt actgg agctggacca gcggaccac ttccccagt 1620
tctctactc gccagcatc cgcgagttag cagtctgcc acgcagagga cgcacgctcg 1680
ctgccatcac cgctgggtgg ttttttacc ctgcc 1715
```

<210> 255

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(431)

<223> 5' terminal sequence. s100 calcium-binding  
protein, beta (neural) (S100B) gene.

<400> 255

```
gagaggatgt ctgagctgga gaaggccatg gtggcctcat cgacgttttc caccaatatt 60
ctggaaggga gggagacaag cacaagctga agaaatccga actcaaggag ctcatcaaca 120
atgagctttc ccatttctta gaggaatca aagagcagga ggttgtggac aaagtcatgg 180
aaacactgga caatgatgga gacggcgaat gtgacttcca gggaattcat ggcctttgtt 240
gccatggtta ctactgcctg ccacgagttc ttggaacat g agtnagatta ggaaagcagc 300
caaacctttt cctgttaaca gaggacggtt catggcaaga naggcaggac aggcaagggg 360
tttgacggct tagttaggga gcttgagggt tttccagccg tntttnttg gttaatttag 420
ggaaggtttg a 431
```

<210> 256

167/292

<211> 1095  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1095)  
<223> s100 calcium-binding protein, beta (neural)  
(S100B) gene.

<400> 256  
tgccgcccag gacccgcagc agagacg acg cctgcagcaa ggagaccagg aaggggtgag 60  
acaaggaaga ggaagtctga gctggagaag gccatggtgg ccctcatcga cgttttccac 120  
caatattctg gaaggaggag agacaagcac aagctgaaga aatccgaact caaggagctc 180  
atcaacaatg agctttccca tttcttagag gaaatcaaag agcaggaggt tgtggacaaa 240  
gtcatggaaa cactggacaa tgatggagac ggcgaaatgtg acttcagga attcatggcc 300  
tttggtgccca tggttactac tgcctgccac gagttctttg aacatgagtg agattagaaa 360  
gcagccaaac ctttcctgta acagagacgg tcatgcaaga aagcagacag caagggcttg 420  
cagcctagta ggagctgagc tttccagccg tgttgtagct aattagga ag cttgatttgc 480  
tttgtagattg aaaaattgaa aacctcttc caaaggctgt ttaacggcc tgcattcttc 540  
tttctgctat attaggctg tgtgtaagct gactggcccc agggactctt gttaacagta 600  
acttaggagt caggtctcag tgataaagcg tgcaccgtgc agcccgccat ggccgtgtag 660  
accctaaccg ggagggaacc ctgact acag aaattacccc ggggcaccct taaaacttcc 720  
actaccttta aaaaacaaag ccttatccag cattatttga aaacactgct gttctttaa 780  
tgcgttcctc atccatgcag ataacagctg gttggccggt gtggccctgc aagggcggtg 840  
tggtctcggc ctgcttcccg ggatgcgcct gatcaccagg tgaacgctca gcgctggcag 900  
cgctctggaa aaagcaactc catcagaact cgcaatccga gccagctctg ggggctccag 960  
cggtggcctcc gtgacccatg cgattcaagt cgcggtgca ggatccttgc ctccaacgtg 1020  
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gcgttcaata aaaag 1095

<210> 257  
<211> 542  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(542)  
<223> 3' terminal sequence. atp -binding cassette,  
sub-family b (mdr/tap), member 1 (ABCB1) gene.

<400> 257  
ttttaaaatc tactttaatt ctgttataaa atttataatg cagttttaaac tatgatttct 60  
ctccacttga tgatgtctct cactctgttc ctttaattac gaagtctctg aagactctga 120  
acttgactga ggaaatgtta aacagatacc tcttcataat tctgtaagtgt tttgctttta 180  
actttgaata aatgtcatat ctaaacaaat attaaaaagt atttaacatc tcatacagtc 240  
agagttcact ggcgctttgt tccagcctgg aactgacca ttgaaaaata gatgcctttc 300  
tgtgccagca gctgctgatg cgtgccatgc tccttgactc tgccattctg aaacaccact 360  
attaagtctg cattctggat ggtggacagg cgttgagcaa tcacaatgca ggtgcggcct 420  
tctctggcta tgccagggct tcttgacaaa ctttttacc tactgtatcc agagctgacg 480  
tggtctatcc aaaagcaaaa tantgggctg tctaacaagg gcacgagcta ttgcatgcg 540  
tt 542



<210> 258  
<211> 4643  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(4643)  
<223> atp-binding cassette, sub-family b  
(mdr/tap), member 1 (ABCB1) gene.

<400> 258  
cctactctat tcagatattc tccagatt cc taaagattag agatcatttc tcattctcct 60  
aggagtactc acttcaggaa gcaaccagat aaaagagagg tgcaacggaa gccagaacat 120  
tcctcctgga aattcaacct gtctcgaggt ttctcgagga atcagcattc agtcaatccg 180  
ggccgggagc agtcatctgt ggtgaggctg attggctggg caggaacagc gccggggcgt 240  
gggctgagca cagcgcttcg ctctctttgc cacaggaagc ctgagctcat tcgagtagcg 300  
gctcttccaa gctcaaagaa gcagaggccg ctgttcgttt cctttaggtc tttccactaa 360  
agtcggagta tcttcttcca agatttcacg tcttggtggc cgttccaagg agcgcgagg 420  
cgggatggat cttgaagggg accgcaatgg aggagcaaag aagaagaac t tttttaaaact 480  
gaacaataaa agtgaaaaag ataagaagga aaagaaacca actgtcagtg tattttcaat 540  
gtttcgctat tcaaattggc ttgacaagtt gtatatggtg gtgggaactt tggctgccat 600  
catccatggg gctggacttc ctctcatgat gctgggtgtt ggagaaatga cagatatctt 660  
tgcaaatgca ggaattttag aagatct gat gtcaaacatc actaatagaa gtgatatcaa 720  
tgatacaggg ttcttcatga atctggagga agacatgacc aggtatgcct attattacag 780  
tggaattggt gctggggtgc tgggtgctgc ttacattcag gtttcatttt ggtgcctggc 840  
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gataggctgg tttgatgtgc acgatgttg ggagcttaac acccgactta cagatgatgt 960  
ctccaagatt aatgaaggaa ttggtgacaa aattggaatg ttctttcagt caatggcaac 1020  
atttttcact ggttttatag taggatttac acgtgggttg aagctaacc ttgtgatttt 1080  
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tgacaccctg gttggagaga gaggggcca gttgagtgtt gggcagaagc agaggatgc 2040  
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aatggaggc ctgcaaccag catttgcaat aatattttca aagattatag gggtttttac 2640  
aagaattgat gatcctgaaa caaacgcaca gaatagtaac ttgttttcac tattgtttct 2700

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tgtgagttgg tttgatgacc ctaaaaacac cactg gagca ttgactacca ggctcgccaa 2880
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tgctcagagt ttgcaggtag catacagaaa ctctttgagg aaagcacaca tctttggaat 3240
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cagtcaagtt cagagtcttc agagacttcg taattaaagg aacagagtga gagacatcat 4440
caagtggaga gaaatcatag tttaaaactgc attataaatt ttataacaga attaaagtag 4500
attttaaaag ataaaatgtg taattttgtt tataatttcc catttggtgact gtaactgact 4560
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taataaaact aaactttcat gtc 4643

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&lt;210&gt; 259

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(486)

<223> 3' terminal sequence. selectin e  
(endothelial adhesion molecule 1) (SELE) gene.

&lt;400&gt; 259

```

caacctttat agtgttatgt caaataggct tgacataagc tttaaataaat atatacttta 60
aaaattataa aatattttta gttataattt aaaattctca ataaaaactca aacacaaacc 1 20
acactgggat ttcacacagc taattttctaa tgcagtttac ataaatattt acaacactta 180
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ctcttatttc ccagagtttt tctgcccctt taaaaggaa ctctggctgt tctgancctt 300
atcacatctc tgttttgact gttgggcttt gggttggtgc cagtgggttc gccaggaaact 360
tctctgggaa actttttttt tcaacactgg ctagggtang gggngttagt gggggngngt 420
ttggtttcnt cacantocct cagggtnggg ggcgggttng gggnattacc ggcggggngt 480
tttttc 486

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<210> 260  
<211> 478  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(478)  
<223> 5' terminal sequence. selectin e  
(endothelial adhesion molecule 1) (SELE) gene.

<400> 260  
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ttcgacagct gattacacag ttcctgtcat aaggaatgaa taattaatta tccagagttt 360  
agaggaaaaa aatgactaaa aatattatta acttaaaaaa tggacaggtg ttggatgccc 420  
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<210> 261  
<211> 3834  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3834)  
<223> selectin e (endothelial adhesion molecule 1)  
(SELE) gene.

<400> 261  
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ttgcttcaca gttctctca gctctcactt tgggtgcttct cattaaagag agtggagcct 180  
ggtcttaca cacctccacg gaa gctatga cttatgatga ggccagtgtc tattgtcagc 240  
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tattgagcta ttcaccaagt tattactgga ttggaatcag aaaagtcaac aatgtgtggg 360  
tctgggtagg aaccagaaa cctctgacag aagaagccaa gaactgggct ccaggtgaac 420  
ccaacaatag gcaaaaagat gaggactgcg tggagatcta catcaagaga gaaaaagatg 480  
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cctgtacca tacatcctgc agtggccacg gtgaatgtgt agagaccatc aataattaca 600  
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 tgttttaaat ttatttcaaa aagggaact attgtcccct agcaaggcat ga tgttaacc 2820  
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&lt;210&gt; 262

&lt;211&gt; 267

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(267)

 <223> 3' terminal sequence. epidermal growth  
 factor (beta-urogastrone) (EGF) gene.

&lt;400&gt; 262

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172/292

```

aaaacaaatc aggcaattta cttacaatct tgtaactgaa aatacatata aattctgtgc 120
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aagcctcctg tgtaatatct taaaatanaa tgttttcatt caaatatttt aaaaaataag 240
natctaactc gaaaaaatca gtttcta                                267

```

&lt;210&gt; 263

&lt;211&gt; 383

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(383)

<223> 5' terminal sequence. protein kinase c  
substrate 80 k-h (PRKCSH) gene.

&lt;400&gt; 263

```

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tncgcacctc cgacgagcag acgcaggcct tcatcgatgc tgcccaggag gcccgcaaca 120
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tacgagctca ccaccaacga atacgtctac cgcctctncc ccttcaagct tgtnttcgna 300
gaaacccaaa ctcgggggct ctcccaccag ccttggcacc tgggggcttc atgggattgg 360
gcccgacca cnacaatttc agt                                383

```

&lt;210&gt; 264

&lt;211&gt; 2056

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2056)

<223> protein kinase c substrate 80k -h (PRKCSH)  
gene.

&lt;400&gt; 264

```

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cagagcgtct ggtgagatgc tgttgccgct gctgctgctg ctacccatgt gctgggccgt 180
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```

173/292

```

catcagggac aagtaccggt ccgaggcact gccaccgac cttccagcac cttctgcccc 1020
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atgtgatccc ccaccc 2056

```

&lt;210&gt; 265

&lt;211&gt; 379

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence :primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(379)

<223> 5' terminal sequence. diphtheria toxin  
receptor (heparin-binding epidermal growth  
factor-like growth factor) (DTR) gene.

&lt;400&gt; 265

```

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cactctatga gttggacttc agtcttgccct aggcgatttt gtctaccatt tgtgttttga 180
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tgccaagtct cagaagaggg tgggctt cca tgcctgtagc tttcctggtc cctcaccccc 300
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aactcctgnc attcttctg 379

```

&lt;210&gt; 266

&lt;211&gt; 2360

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2360)

<223> diphtheria toxin receptor (heparin-binding  
epidermal growth factor-like growth factor) (DTR)  
gene.

&lt;400&gt; 266

```

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gctgcagttc tctcggcact ggtgactggc gagagcctgg agcggcttcg gagagggcta 360
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&lt;210&gt; 267

&lt;211&gt; 435

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(435)

&lt;223&gt; 5' terminal sequence. integrin, beta 2

(antigen cd18 (p95), lymphocyte

function-associated antigen 1; macrophage antigen

1 (mac-1) beta subunit) (ITGB2) gene.

&lt;400&gt; 267

```

aggagtcccc cggtgcccc tcacctgtg gcaagtacat ctctgcgcc gagtgcctga 60

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ctacacgctg gagcagcagg acgggatgga ccgctacctc atctatgtgg atgagagccg 240  
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ccctttttca agagc 435

<210> 268

<211> 2776

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2776)

<223> integrin, beta 2 (antigen cd18 (p95),  
lymphocyte function-associated antigen 1;  
macrophage antigen 1 (mac -1) beta subunit) (ITGB2)  
gene.

<400> 268

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cctgactcca ttcgctgcga caccggcca cagc tgctca tgaggggctg tgcggtgac 300  
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```

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aaaataaaac ttcaat 2776

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&lt;210&gt; 269

&lt;211&gt; 449

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(449)

<223> 5' terminal sequence. neogenin (chicken)  
homolog 1 (NEO1) gene.

&lt;400&gt; 269

```

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tctaggggaag ggagccggcc tcctatgcca gtggttggtc ccagtgcctc t gaagtgcag 300
ggagaccaca aggtgtttg gaaggattnc gagagtaggt attgaaccag ntgaggttga 360
ncaaagagtt gggccatngg gggaggggatt aattgaangg gaccttaaac gtttttnac 420
aacagcttga cggactttta acggggggc 449

```

&lt;210&gt; 270

&lt;211&gt; 5297

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(5297)

&lt;223&gt; neogenin (chicken) homolog 1 (NEO1) gene.

&lt;400&gt; 270

```

gggcccggcc gggctgggct ggagcagcgg cgcccgggag ccgagcttgc agcgagggac 60
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tctggtggag ccggtggata cactctcagt tagaggctct tctgttatat taaactgttc 360
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agtatcagat gatcgacgcc agcttctccc ggatggatct ttatttatca gcaatgtggt 480

```

gcattccaaa cacaataa ac ctgatgaagg ttattatcag tgtgtggcca ctgttgagag 540  
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 tgatagagtt atcaaaacttc caagtggAat gctggttatc agcaatgcaa ctgaaggaga 780  
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 cagtcatctc taccaccogg gcagcccatg gccattggc acatccatgt cctttcaga 4020  
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cttgccagc tcccaagagg aagattcagg ccagagtctt ccca ctgccc atgttcgccc 4200
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5297

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&lt;210&gt; 271

&lt;211&gt; 389

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(389)

<223> 3' terminal sequence. pou domain, class 2,  
transcription factor 2 (POU2F2) gene.

&lt;400&gt; 271

```

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ccctcttgcc tgaaatttcc accttcccat aggtctggga gggagtcagt tccagagcag 120
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cccacccttc aaaggggaaa agagggagga acaggggatg aaaagttntc cgcagccttc 240
ccttgaactc tcccctgctg ggggagggag gaggttaaag caagaccccc tgcccaggtg 300
gggagagctg ggggccaggg gagaagggga caaatggtag ggacacattc tgtttgagca 360
caatgctaaa aattctgtac atcctttgg
389

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&lt;210&gt; 272

&lt;211&gt; 2048

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2048)

<223> pou domain, class 2, transcription factor 2  
(POU2F2) gene.

&lt;400&gt; 272

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```
cgtaacatg agttgggctt ggggcagatg aggctggctg gcggggcggg cagcatggtt 60
cactccagca tgggggctcc agaaataaga atgtctaagc ccctggaggc cgagaagcaa 120
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tgaaaaaaca aaaaaaaa ccaaaaaa accaaaaaa aaaaaaac tctaccctc 2040
ctagagcc 2048
```

&lt;210&gt; 273

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(472)

<223> 3' terminal sequence. baculoviral iap  
repeat-containing 4 (BIRC4) gene.

&lt;400&gt; 273

```
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tgattgggga gattaactct aatctccaca tttatataca gaaagctcca tttgttaagc 120
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ggtttcaatt aaataacagt aaaaaaatg gataatacag ctaataccct gaaaaatcaa 300
gaaattcaaa gattatattg ccaactaaaa cactgccatg tacatttttt ttctacttg 360
gtagcaaatg ctaatggaat tcaatcctga ttacttaaag tcagttcaca tcacacattc 420
aatcagggta ataagaacaa cataacatgc ctaccataga gttagatta a ga 472
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<210> 274  
<211> 2540  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2540)  
<223> baculoviral iap repeat -containing 4 (BIRC4)  
gene.

<400> 274  
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ttaaaaaactt ttgctaattt tccaagtggg agtcctgttt cagcatcaac actggcacga 180  
gcagggtttc tttatactgg tgaaggagat accgtgcggt gcttt agttg tcatgcagct 240  
gtagatagat ggcaatatgg agactcagca gttggaagac acaggaaagt atccccaaat 300  
tgcagattta tcaacggctt ttatcttgaa aatagtgcc cgcagctctac aaattctgtg 360  
atccagaatg gtcagtacaa agttgaaaac tatctgggaa gcagagatca ttttgcctta 420  
gacaggccat ctgagacaca tgc agactat cttttgagaa ctgggcaggt tgtagatata 480  
tcagacacca tatacccgag gaacctgcc atgtattgtg aagaagctag attaaagtcc 540  
tttcagaact ggccagacta tgctcaccta accccaagag agttagcaag tgctggactc 600  
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gagatatgtt aagtgtaaaa t gcaagtggc gggacactat gtatagtctg agccagatca 2220  
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ttaaatgtgg tttctcttcg gggagggggg gattggggga ggggccccag aggggtttta 2340  
gaggggcctt ttacttttcg acttttttca ttttgttctg ttoggatttt ttataagtat 2400  
gtagaccocg aagggtttta tggaactaa catcagtaac ctaaccccg tgactatcct 2460  
gtgctcttcc tagggagctg tgtgttttcc caccaccac ccttccctct gaacaaatgc 2520  
ctgagtgtcg gggcactttg 2540

181/292

<210> 275  
<211> 842  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(842)  
<223> 3' terminal sequence. death associated  
protein 3 (DAP3) gene.

<400> 275  
tagaaagata ttttattttt taggaaaaga gccataatta tcttaaa tgt gaaaaaccac 60  
atccaataaa ctgatataaa gttttaggaa caagggaata tcttattgtc acgcattcac 120  
agtgaacccc attttaatgc aggtccagag ccaactgcag tcctgtccaa tcccataggt 180  
acaagggcct ggctcctctt cctgtgtact gcccgacttc ctcatcttac tgggtccagc 240  
ataaagcaga tgtccactgt ctctct caca tgctgtgatc ttggcttaga ggtaggcaca 300  
gtgccgctcc agcagcgagg ggttcgcgtt acttaggaac agcagctctt tttcccttc 360  
ttctgtagga gctntctcat gttgaagcca attgttttcc aaataatact gaatacaact 420  
ttcaaattcc tttgggttat agttggaac caggatggga ataaagggat ccagggcac 480  
aaatccttcc tttccagca actcctgcgg cagataggct ttccggggct taaagagaga 540  
cccagctcgg ctacagaccg acacaatggc gcctccatgc caatcatnct tcatcatttt 600  
cctcagttgt gaacaagtgc taattccctc ggggcaatcg ggctttatct tctgttttca 660  
gagggttctt cccaangag cattgatgcc accacggcca cctatg ggtg aaacataccc 720  
caatgaactt tgctcttttag ctctttcagc acaatttcaa actgatctgg tgcgtccctc 780  
aaccgtgtta tgccctgtca aaccacttct ccagaagac tccctttctt aggttttct 840  
ct 842

<210> 276  
<211> 1608  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1608)  
<223> death associated protein 3 (DAP3) gene.

<400> 276  
gaattccgcc ggccccaggc agcgtgtgtc ggtgcctag gctggagaac tagtct cga 60  
ctcacgtgca aggatgatgc tgaaaggaat aacaaggctt atctctagga tccataagtt 120  
ggaccctggg cgttttttac acatggggac ccaggctcgc caaagcattg ctgctcacct 180  
agataaccag gttccagttg agagtccgag agctatttcc cgcaccaatg agaatgacct 240  
ggccaagcat ggggatcagc acgaggggtca gcacta caac atctcccccc aggatttgga 300  
gactgtattt ccccatggcc ttctcctcg ctttgtgatg caggtgaaga cattcagtga 360  
agcttgctg atggttaagga aaccagccct agaactctg cattacctga aaaacaccag 420  
tttgcttat ccagctatac gatattctct gtatggagag aagggaacag gaaaaaccct 480  
aagtctttgc catgttattc atttctgtgc aaaacaggac tggctgatac tacatattcc 540  
agatgctcat ctttgggtga aaaattgtcg ggatcttctg cagtcagct acaacaaaca 600  
gcgctttgat caacctttag aggtttcaac ctggctgaag aatttcaaaa ctacaaatga 660  
gcgttctctg aaccagataa aagttcaaga gaagtatgtc tggaataaga gagaaa gcac 720  
tgagaaaggg agtctctgga gagaagtggg tgaacagggc ataacacggg tgaggaacgc 780  
cacagatgca gttggaattg tgctgaaaga gctaaagagg caaagttctt tgggtatgtt 840  
tcacctcta gtggcgtg atggaatcaa tgctctttgg ggaagaacca ctctgaaaag 900

```

agaagataaa agccccgattg cccccgagga atta gcactt gttcacaact tgaggaaaat 960
gatgaaaaat gattggcatg gaggcgccat tgtgtcggct ttgagccaga ctgggtctct 1020
ctttaagccc cggaagcct atctgccccca ggagttgctg ggaaaggaag gatttgatgc 1080
cctggatccc tttattocca tcctggtttc caactataac ccaaaggaat ttgaaagttg 1140
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gaaaaaagag ctgctgttcc taagtaacgc gaacccctcg ctgctggagc ggcactgtgc 1260
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acccagtaag atgaggaagt cgggcagtac acaggaagag gagccagc c cttgtacct 1380
tgggattgga caggactgca gttggctctg gacctgcatt aaaatgggtt tcactgtgaa 1440
tgcgtagcaa taagatatc cctgttcct aaaactttat atcagtttat tggatgtgt 1500
ttttcacatt taagataatt atggctctt tcctaaaaaa taaaatatct ttctaaaaaa 1560
aaaaaaaaa aaaaaaaaaa aaa aaaaaaa aaaaaaaaaa aaaaaaa 1608

```

&lt;210&gt; 277

&lt;211&gt; 361

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(361)

<223> 5' terminal sequence. gonadotropin-releasing hormone 1 (leutinizing-releasing hormone) (GNRH1) gene.

&lt;400&gt; 277

```

ttagattgca tgctattgta tgtctacagg gcatttgaca gccaaggnt aaatccaggt 60
gggacgtat ctaatgatgt cctgtccttc actgtccttg ccatcaccag ccacagagat 120
ccaggctttg gggactccca cagcttatcg accag tgttt gatttagttt ttagcctctt 180
tcccatcaaa tgaaaattaa cttggagaca catttcatta gaaaattaga ggcccccttg 240
gctaggaagg catctggtct ggggactaac tactttgaac agtgttgagt cctctctccc 300
acagatgggt cagccagcag taatgctnag ggaagactga agggatcaaa taganaaatg 360
t 361

```

&lt;210&gt; 278

&lt;211&gt; 470

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(470)

<223> gonadotropin-releasing hormone 1 (leutinizing-releasing hormone) (GNRH1) gene.

&lt;400&gt; 278

```

gggatctttt tggtctctctg cctctaaaca gaatgaagcc aattcaaaaa ctctagctg 60
gccttattct actgacttgg tgcgtggaag gctgtccag ccagcactgg tcctatggac 120
tgcgccctgg aggaagaga gatgccgaaa atttgattga ttctttcca a gagatagtca 180
aagaggttgg tcaactggca gaaacccaac gcttcgaatg caccacgcac cagccacgtt 240
ctccccctcg agacctgaaa ggagctctgg aaagtctgat tgaagaggaa actgggcaga 300
agaagattta aatccattgg gccagaagga atgaccatta ctaacatgac ttaagtataa 360
ttctgacatt gaaaatttat aacccat taa atacctgtaa atggtatgaa tttcagaaat 420

```

ccttacacca agttgcacat attccataat aaagtgcctgt gttgtgaatg

470

&lt;210&gt; 279

&lt;211&gt; 320

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(320)

<223> 3' terminal sequence. interleukin 2  
receptor, gamma (severe combined immunodeficiency)  
(IL2RG) gene.

&lt;400&gt; 279

ntctaaatat caacagaaac tttatttctc atcggttcag gaacaatcgg agggtagatg 60  
gaaagaggaa gggagggaaa gagggaggga ggaagaatcc tgcgaaaagg aagggccaga 120  
ctgaggggaga agaaaaacat gttcggggca aaagggtaat totcaagtgg ggaatgccaa 180  
atgaaggggt gcttacatgg gggcacaaaa ttccaaatca gccacagtgg ggtgagggtga 240  
gtatgagacg caggtggggt tgaatgaagg aaagttagta ccncttaggg ctacaggacc 300  
ctggggttct tctttcag ag 320

&lt;210&gt; 280

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(407)

<223> 5' terminal sequence. interleukin 2  
receptor, gamma (severe combined immunodeficiency)  
(IL2RG) gene.

&lt;400&gt; 280

attcggcaca gggaactttt cggcctggag tgggtgtgtct aagggaactgg ctgagagtct 60  
gcagccagac tacagtgaac gactctgcct cgtcagttag attccccaa aaggaggggc 120  
ccttggggag gggcctgggc tncctcatgc aaccagcata gccctactg ggcccccca 180  
tggtacaccc taaagcctga aacctgaacc ccantactct gacagaagaa cccaggggtc 240  
ctgtagccct aagtggtagt aactttcctt cattcaaccc acctgcgtct tatactcanc 300  
tcanccact gttggctgat tttggatttt tgtggcccca tgtaaggaac cctttaattt 360  
ggcattnccc aattgagaat taaccttttt gncccaaca tggtttt 407

&lt;210&gt; 281

&lt;211&gt; 1451

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;



<221> misc\_feature  
<222> (1)..(1451)  
<223> interleukin 2 receptor, gamma (severe  
combined immunodeficiency) (IL2RG) gene.

<400> 281  
gaagagcaag cgccatgttg aagccatcat taccattcac atccctctta ttcctgcagc 60  
tgcccctgct gggagtgggg ctgaacacga caattctgac gcccaatggg aatgaagaca 120  
ccacagctga tttcttctctg accactatgc ccactgactc cc tcagtgtt tccactctgc 180  
ccctcccaga ggttcagtgt tttgtgttca atgtcgagta catgaattgc acttgggaaca 240  
gcagctctga gcccagcct accaacctca ctctgcatta ttggtacaag aactcggata 300  
atgataaagt ccagaagtgc agccactatc tattctctga agaaatcact tctggctgtc 360  
agttgcaaaa aaaggagatc cacctctacc aaacatttgt tgttcagctc caggaccac 420  
gggaacccag gagacaggcc acacagatgc taaaactgca gaatctggtg atccctggg 480  
ctccagagaa cctaacactt cacaactga gtgaatccca gctagaactg aactggaaca 540  
acagattctt gaaccactgt ttggagcact tgggtgcagta cgggactgac tgggaccaca 60 0  
gctggactga acaatcagtg gattatagac ataagttctc cttgcctagt gtggatgggc 660  
agaaacgcta cacgtttcgt gttcggagcc gctttaacc cactctgtgga agtgctcagc 720  
attggagtga atggagccac ccaatccact gggggagcaa tacttcaaaa gagaatcctt 780  
tctgtttgc attggaagcc gtggttatct ctggttgctc catgggattg attatcagcc 840  
ttctctgtgt gtatttcttg ctggaacgga cgatgcccg aattcccacc ctgaagaacc 900  
tagaggatct tgttactgaa taccacgga acttttcgga ctggagtggg gtgtctaagg 960  
gactggctga gagtctgcag ccagactaca gtgaacgact ctgectcgtc agtgagattc 1020  
ccccaaaagg agggcccctt ggggaggggc ctggggcctc cccatgcaac cagcatagcc 1080  
cctactgggc cccccatgt tacaccctaa agcctgaaac ctgaaccca atcctctgac 1140  
agaagaaccc cagggtcctg tagccctaag tggactaac tttccttcat tcaaccacc 1200  
tgcgctcat actcacctca cccactgtg gctgatttg aattttgtgc ccccatg taa 1260  
gcaccccttc atttggcatt cccacttga gaattacct tttgcccga acatgttttt 1320  
cttctccctc agtctggccc ttcttttctg caggattctt cctccctccc tctttcctc 1380  
ccttctctt tccactacc ctccgattgt tctgaaccg atgagaaata aagtttctgt 1440  
tgataatcat c 1451

<210> 282  
<211> 317  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(317)  
<223> 3' terminal sequence. death associated  
protein 3 (DAP3) gene.

<400> 282  
atctaacaca acactttaga aagatatttt attttttagg aaaagagcca taattatctt 60  
aaatgtgaaa aaccacatcc aataaactga tataaagttt taggnacaag ggaatatctt 120  
attgtcacgc attcacagt aaacccattt taatgcaggt ccagagccaa ctgcagtcc 180  
gtccaatccc atagggtaga agggcctggg ctctcttcc tgtgtactgc ccgacttcc 240  
catcttactg gggccagca taaagcagga tgcactgt ctctctcaca tgctgtganc 300  
ttggncttag gagtag 317

<210> 283  
<211> 358  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(358)

&lt;223&gt; 5' terminal sequence. death associated protein 3 (DAP3) gene.

&lt;400&gt; 283

```
aggacgggcg ctttggagcc ggccccaggc agcgtgtgtc ggtcgcctag tctggagaac 60
tagtcctcga ctcacgtgca aggatgatgc tgaaaggaat aacaaggcctt atctctagga 120
tccataagtt ggaccctggg cgttttttac acatggggac ccaggctcgn caaagcattg 180
ctgctcacct agataacca ggttcccagt tgagagtccc gagagctatt ttcccgaac 240
caatgagaat gaccccggcc caagcatggg ggatcancaa ggagggtcaa gcaa tnacaa 300
canttttccc cccaggattt tgggagaatt gtaattttcc ccatinggcct ttncttcc 358
```

&lt;210&gt; 284

&lt;211&gt; 416

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(416)

&lt;223&gt; 5' terminal sequence. ptk2 protein tyrosine kinase 2 (PTK2) gene.

&lt;400&gt; 284

```
gcacagaagc tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccag 60
cagtatgtca tgaccgcct ccagcaagag tacaaaaagc aaatgctgac tgctgctcac 120
gccctggctg tggatgcaa aaacttactc gatgtcattg a ccaagcaag actgaaaatg 180
cttgggcaga cgagaccaca ctgagcctcc cctaggagca cgtcttgcta cctcttttg 240
aagatgttct ctagccttcc accagcagcg agganttaac cctgtgtcct cagtncgcca 300
gcacttacag ctccaacttt tttgaatgac catctggttg aaaaatcttt ctcatataag 360
tttnaaccac atttggattt ggggttcatt ttttgtttg ttttttttc aatcat 416
```

&lt;210&gt; 285

&lt;211&gt; 3052

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3052)

&lt;223&gt; ptk2 protein tyrosine kinase 2 (PTK2) gene.

&lt;400&gt; 285

```
ccggtgtgaa ggccatgagt gattactggg ttgttgaaa gaagtctaac tatgaagtat 60
tagaaaaaga tgttggttta aagcgatttt ttctaagag tttactggat tctgtcaagg 120
ccaaacact aagaaaactg atccaacaaa catttagaca atttgccaac ctaaatagag 180
aagaaagtat tctgaaattc tttgagat cc tgtctccagt ctacagattt gataaggaa 240
gttcaagtgt tgctcttggg tcaagctgga ttatttcagt ggaactggca atcggccag 300
```

186/292

```

aagaaggaat cagttaccta acggacaagg gctgcaatcc cacacatctt gctgacttca 360
ctcaagtgcga aaccattcag tattcaaaaca gtgaagacaa ggacagaaaa ggaatgctac 420
aactaaaaat agcagggtgca cccgagcctc tgacagtgcg ggcacccatcc ctaaccattg 480
cggagaatat ggctgaccta atagatgggt actgccggct ggtgaatgga acctgcagct 540
catttatcat cagacctcag aaagaagggt aacgggcttt gccatcaata ccaaagttgg 600
ccaacagcga aaagcaaggc atgcgggacac acgcccgtctc tgtgtcag aa acagatgatt 660
atgctgagat tatagatgaa gaagatactt acaccatgcc ctcaaccagg gattatgaga 720
ttcaaaagaga aagaatagaa cttggacgat gtattggaga aggccaattt ggagatgtac 780
atcaaggcat ttatatgagt ccagagaatc cagctttggc ggttgcaatt aaaacatgta 840
aaaactgtac ttcgagacgc gtgaga gaga aatttcttca agaagcctgc cattacacat 900
ctttgcactg gaattgggtgc agatatataa gtgacccata tgttgatgcc tgcccagacc 960
ccaggaatgc agagttaaca atgcgctcag ttgacctacc tcatattgtg aagctgattg 1020
gagtcacac agagaatcct gtctggataa tcatggagct gtgcacactt ggagagctga 1080
ggtcattttt gcaagtaagg aaatacagtt tggatctagc atctttgatc ctgtatgcct 1140
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ctgctcggaat tggtctgggt tcctcaaatg atttgttaaa attaggagac tttggattat 1260
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ggatggctcc agagtcaatc aattttcgac gttttacctc agctagtgc gtatggatgt 1380
ttgggtgtgt tatgtgggag atactgatgc atgggtgtgaa gccttttcaa ggagtgaaga 1440
acaatgatgt aatcggtcga attgaaaatg gggaaagatt accaatgcct ccaaattgtc 1500
ctcctaccct ctacag cctt atgacgaaat gctgggccta tgacccagc agggcgcca 1560
ggtttactga acttaaagct cagctcagca caatcctgga ggaagagaag gctcagcaag 1620
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ctgatgaagc accgcccag cccagcagac cgggttatcc cagtcaggag tccag cgaag 1740
gattttatcc cagcccacag cacatggtac aaaccaatca ttaccagggt tctggctacc 1800
ctggttcaca tggaatcaca gccatggctg gcagcatcta tccaggtcag gcactcttt 1860
tggaccaaac agattcatg aatcatagat ctcaggagat agcaatgtg cagcccaatg 1920
tggaggactc tacagtattg gacctgcgag ggattgggca agtgttgcca acccatctga 1980
tggaagagcg tctaaccga cagcaacagg aaatggaaga agatcagcgc tggctggaaa 2040
aagaggaaag atttctgatt ggaaaccaac atatatatca gcctgtgggt aaaccagatc 2100
ctgcagctcc accaaagaaa ccgcctcgcc ctggagctcc cggtcactctg ggaagccttg 2160
ccagcctcag cagccctgct gacagctaca acgaggggtgt caagcttcag cccaggaaa 2220
tcagccccc tcctactgcc aacctggacc ggtcgaatga taagggtgtac gagaatgtga 2280
cgggcctgggt gaaagctgtc atcgagatgt ccagtaaaat ccagccagcc ccaccagagg 2340
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tattgaaact tgacctgggt gagctcatca caagatgaa actggcccag cagtatgtca 2520
tgaccagcct ccagcaagag tacaaaaagc aaatgctgac tgccgctcac gccctggctg 2580
tggatgcaa aaacttac tc gatgtcattg accaagcaag actgaaaatg cttgggcaga 2640
cgagaccaca ctgagcctcc cctaggagca cgtcttgcta cctcttttg aagatgttct 2700
ctagccttcc accagcagcg aggaattaac cctgtgtcct cagtcgccag cactcacagc 2760
tccaactttt ttgaatgacc atctggttga aaaacttttc tcatataagt ttaacca cac 2820
tttgatttgg gttcattttt tgttttgggt ttttcaatca tgatattcag aaaaatccag 2880
gatccaaaat gtggcggttt tctaagaatg aaaattatat gtaagctttt aagcatcatg 2940
aagaacaatt tatgttcaca ttaagatacg ttctaaagg ggtggccaa ggggtgacat 3000
cttaattcct aaactacctt agctgcatag t ggaagagga gagccgaat tc 3052

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&lt;210&gt; 286

&lt;211&gt; 377

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(377)

<223> 3' terminal sequence. cyclin-dependent  
kinase 4 (CDK4) gene.

&lt;400&gt; 286

```
gnataaaaaa ggaccccaaa tataaaggna gggaaaggga caagagggaa catacccctt 60
agtgtagaga aatgggaagg agaaggagaa gcctcaaaag gaggtgggag gggaatgtca 120
ttaaggcagc aaagtaatct ctgtagaaag atggaggagg accctocata gcctcagaga 180
taaaggcaaa gattgccctc tc agtgtcca gaagggaat gggcagcttt tcttccttcc 240
atgggcagcc actccattgc tcaactccgn ttaccttcat ccttatgtag gataagagtn 300
ctgcagagct tcgaaagggc agagattcgc ttgtgtggg ttaaaagtca gcatttccan 360
cagcagcttt tgcttcc 377
```

&lt;210&gt; 287

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(363)

<223> 5' terminal sequence. cyclin-dependent  
kinase 4 (CDK4) gene.

&lt;400&gt; 287

```
catatctgga caaggcacc ccaccaggct tgcagccgaa acgatcaagg atctgatgcg 60
ccagtttcta agaggcctag atttccttca tgccaattgc atcggtcacc gagatctgaa 120
gccagagaac attctggtga caagtgtng aacagtcaag ctggctgact ttngcctggc 180
cagaatctac agctaccaga tggcacttac acccgtggtt gttacactct ggtacc gagg 240
tcccgaagtt cttctngcag tccacatatg caacacctgt gggacatgtg ggagtgttgg 300
ctgtatcttt gcagagatgt ttctgcgaaa ncctctcttt ctgtggnaaa ctctgtaagg 360
ccg 363
```

&lt;210&gt; 288

&lt;211&gt; 1443

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1443)

&lt;223&gt; cyclin-dependent kinase 4 (CDK4) gene.

&lt;400&gt; 288

```
gccctcccag tttccgcgcg cctctttggc agctggtcac atggtgaggg tgggggtgag 60
ggggcctctc tagcttgccg cctgtgtcta tggtcgggcc ctctgcgtcc agctgctccg 120
gaccgagctc ggggtgatgg ggcgtagga accggctccg gggccccgat aacgggccgc 180
ccccacagca ccccgggctg gcgtgagggc ctcccttgat ctgagaatgg ctacctctcg 240
atatgagcca tggctgaaa ttggtgtcgg tgcctatggg acagtgt aca aggccgtga 300
tccccacagt ggccactttg tggccctcaa gagtgtgaga gtccccaatg gaggaggagg 360
tggaggaggc cttcccatca gcacagttcg tgaggtggct ttactgaggc gactggaggc 420
ttttgagcat cccaatgttg tccggctgat ggacgtctgt gccacatccc gaactgaccg 480
ggagatcaag gtaaccctgg tgttt gagca tgtagaccag gacctaaagg catatctgga 540
caaggcacc ccaccaggct tgccagccga aacgatcaag gatctgatgc gccagtttct 600
aagaggccta gatttcctc atgccaattg catcggtcac cgagatctga agccagagaa 660
cattctggtg acaagtgtg gaacagtcaa gctggctgac tttggcctgg ccagaatcta 720
```

188/292

```

cagctaccag atggcactta caccogtggg ttgtacactc tggtagcgag ctcccgaagt 780
tcttctgcag tccacatatg caacacctgt ggacatgtgg agtggttgct gtatctttgc 840
agagatgttt cgtcgaaagc ctctcttctg tggaaactct gaagccgacc agttgggcaa 900
aatctttgac ctgattgggc tgcctccaga ggatgactgg cctcg agatg tatccctgcc 960
ccgtggagcc tttcccccca gagggccccg ccagtgacag tgggtgttac ctgagatgga 1020
ggagtcggga gcacagctgc tgctggaaat gctgactttt aaccacaca agcgaatctc 1080
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gcaatctttg cctttatctc tgaggctatg gagggtcctc ctccatcttt ctacagagat 1260
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ttccatttc tctacactaa ggggtatgtt ccctctgtc cctttcccta cctttatatt 1380
tggggtcctt ttttatagc gaaaaacaaa accaaaagaa awaatggccc tttttttttt 1440
ttt 1443

```

&lt;210&gt; 289

&lt;211&gt; 394

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(394)

<223> 3' terminal sequence. basic transcription  
factor 3 (BTF3) gene.

&lt;400&gt; 289

```

ccgcgtgtg tgcgcctaan ctgagnggn ccaccgaga ccccttgagc accaacccta 60
gtccccgcg cggccctna ttgctccga caagatgaaa gaaaca atca tgaaccaggg 120
aaaactcgcc aaactgcagg cacaagtgcg cattggtggg aaaggaactg ctgcgagaaa 180
gaagaagtg gttcatagaa cagccacagc agatgacaaa aaacttcagt tctccttaaa 240
gangttagg gtaacaata tctctggnat tgaagagggt aatatgttta caaaccaggg 300
aacagtgatc cactttaaca acc tnaagt tcagggcac tctgggcagc ggacactttc 360
accattacng gccttgctga gncaaagcag ctgg 394

```

&lt;210&gt; 290

&lt;211&gt; 477

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(477)

&lt;223&gt; basic transcription factor 3 (BTF3) gene.

&lt;400&gt; 290

```

atgcgacgga caggcgaccc cgctcaggct gactctcggg ggcgaggctg agccaggggc 60
ggctgccctg gggcgaggc gacgtgtct caacctccac ctgcggcgg aaccgagga 120
gaggagcctc agatgaaaga aacaatcatg aaccag gaaa aactcgcaa actgcaggca 180
caagtgcgca ttggtgggaa agtgaatatg ttacaaacc aaggaacagt gatccacttt 240
aacaacccta aagttcaggc atctctggca gcaaacactt tcaccattac aggccatgct 300
gagacaaagc agctgacaga aatgctaccc agcatcttaa accagcttgg tgcggatagt 360
ctgactagtt taaggagact ggccgaagct ctgcccacac aatctgtgga tggaaaagca 420
ccacttgcta ctggagagga tgatgatgat gaagttccag gaggttcca agaata 477

```

<210> 291  
<211> 388  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(388)  
<223> 3' terminal sequence. colony stimulating  
factor 1 receptor, formerly mcdonough feline  
sarcoma viral (v-fms) oncogene homolog (CSF1R)  
gene.

<400> 291  
tgctgttagt ttaatgtgga cagagacatc ccacggcgtg actgttagt t aggatgagtc 60  
agcttggggg agtttgtgct tcctgcttgg nggtggccagc cacatgccaa ggtcccctgc 120  
cttctagccc agaatgacgg gactgggcag aacacccccca acttttagct gccacttggc 180  
tcattacagc agtaccagta tgggggtggg aggggtgagg cnttgagtg aaggcggcgt 240  
atagggcaga gactaagagg gtcctgtg ag attcttagag gagccatcct gntccaagg 300  
gcctgagctg agtntgggtc tgtgagcatc tgctgctcct ctcagagagg ggagatctca 360  
ctctctgccg gctctgtctag ccccaaag 388

<210> 292  
<211> 3992  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3992)  
<223> colony stimulating factor 1 receptor,  
formerly mcdonough feline sarcoma viral (v-fms)  
oncogene homolog (CSF1R) gene.

<400> 292  
ggcttcagga agggcagaca gagtgtccaa aagcgtgaga gcacgaagtg aggagaaggt 60  
ggagaagaga gaagaggaag aggaagagga agagaggaag cggaggggaac tgcggccagg 120  
ctaaaagggg aagaagagga tcagcccaag gaggaggaag aggaaaacaa gacaaacagc 180  
cagtgcagag gagaggaacg tgtgtccagt gtcccgatcc ctgcggagct agtagctgag 24 0  
agctctgtgc cctgggcacc ttgcagccct gcacctgcct gccacttccc caccgaggcc 300  
atgggcccag gagttctgct gtcctgtctg gtggccacag cttggcatgg tcagggaatc 360  
ccagtgatag agcccagtg tcccgagctg gtcgtgaagc caggagcaac ggtgaccttg 420  
cgatgtgtgg gcaatggcag cgtggaatgg gatggccccg catcacctca ctggaccctg 480  
tactctgatg gtcacagcag catcctcagc accaacaacg ctaccttcca aaacacgggg 540  
acctatcgct gcactgagcc tggagacccc ctgggaggca gcgccgcat ccacctctat 600  
gtcaaagacc ctgcccggcc ctggaacgtg ctagcacagg aggtggtcgt gttcgaggac 660  
caggacgcac tactgcctg tctgctcaca gaccgggtgc tggaaagcagg cgtctcgctg 720  
gtgcgtgtgc gtggccggcc cctcatgcgc cacaccaact actccttctc gccctggcat 780  
ggcttcacca tccacagggc caagttcatt cagagccagg actatcaatg cagtgccttg 840  
atgggtggca ggaaggtgat gtccatcagc atccggctga aagtgcagaa agtcatccca 900  
gggccccag ccttgacact ggtgcctgca gagctggtgc ggattcgagg ggaggctgcc 960  
cagatcgtgt gtcagccag cagcgttgat gttaactttg atgtcttcct ccaacacaac 1020

190/292

```

aacactaagc tcgcaatccc tcaacaatct gactttcata ataaccgtta ccaaaaagtc 1080
ctgaccctca acctogatca agtagatttc caacatg ccg gcaactactc ctgcgtggcc 1140
agcaacgtgc agggcaagca ctccacctcc atgttcttcc ggggtggtaga gagtgcctac 1200
ttgaacttga gctctgagca gaacctcatc caggaggtga ccgtggggga ggggctcaac 1260
ctcaaagtca tggtaggggc ctaccaggc ctgcaaggtt ttaactggac ctacctggga 1320
cccttttctg accaccagcc tgagcccaag ctgtctaag ctaccaccaa ggacacatac 1380
aggcacacct tcacctctc tctgccccgc ctgaagccct ctgaggctgg ccgtactacc 1440
ttcctggcca gaaaccagg aggtctggaga gctctgacgt ttgagctcac ccttcgatac 1500
ccccagagg taagcgtcat atggacattc atcaacggct ctggcaccct tttgtgtgct 1560
gcctctgggt acccccagcc caacgtgaca tggctgcagt gcagtggcca cactgatagg 1620
tgtgatgagg cccaagtgtc gcaggtctgg gatgacctat accctgaggt cctgagccag 1680
gagcccttcc acaaggtgac ggtgcagagc ctgctgactg ttgagacctt agagcacaac 1740
caaacctacg atgtcaggcc ccaca acagc gtggggagtg gctcctgggc cttcataccc 1800
atctctgcag gagccacac gcacccccgc gatgagttcc tcttcacacc agtgggtggc 1860
gcctgcatgt ccatcatggc cttgctgctg ctgctgctcc tgctgctatt gtacaagtat 1920
aagcagaagc ccaagtacca ggtccgctgg aagatcatcg agagctatga gggcaacagt 1980
tatactttca tcgacccccc gcagctgcct tacaacgaga agtgggagtt cccccggaac 2040
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gcctttgtgc tgggcaagga ggatgctgct ctgaaggtgg ctgtgaagat gctgaagtcc 2160
acggccccatg ctgatgagaa ggaggccctc atgtccgag c tgaagatcat gagccacctg 2220
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gccatgctgg gacccagcct gagccccggc caggaccccg agggaggcgt cgactataag 2400
aacatccacc tcgagaagaa atatgtccgc agggacagtg gcttctccag ccagggtgtg 2460
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gtgaacagca agttctataa actggtgaag gatggatacc aaatggccca gcctgcattt 2940
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gagctggagg aggagagctc tagtgagcac ctgacctgct gcgagcaagg ggatatcgcc 3180
cagcccttgc tgcagcccaa caactatcag ttctgctgag gaggttgacga cagggagtag 3240
cactctcccc tctccaaaac ttcaactcct ccatggatgg ggcgacacgg ggagaacata 3300
caaaactctg cttcggatcat ttactcaac agctcggccc agctctgaaa cttgggaagg 3360
tgagggatcc aggggaggtc acttctctg agaggatccc catgggccat cactgccagt 3420
caggggctgg gggctgagcc ctacccccgc gcctccccta ctgttctcat ggtgttgcc 3480
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tctttggggc tagacagact ggcagagagt gagatctccc tctctgagag gagcagcaga 3660
tgctcacaga ccacactcag ctccagcccc ttggagcagg atggtcctc taag aatctc 3720
acaggacctc ttagtctctg cctatacgc cgccttcaact ccacagcctc acccctccca 3780
ccccatact ggtactgctg taatgagcca agtggcagct aaaagttggg ggtgttctgc 3840
ccagtcctcg cattctgggc tagaaggcag gggacettgg cattggctgg ccacaccaag 3900
caggaagcac aaactcccc aagctgact c atcctaacta acagtcaagc cgtgggatgt 3960
ctctgtccac attaaactaa cagcattaat gc 3992

```

&lt;210&gt; 293

&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

191/292

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(356)

<223> 3' terminal sequence. friend leukemia virus  
integration 1 (FLI1) gene.

&lt;400&gt; 293

```

tttatttagt caaattatatt tacaacatgg ncttctttga cagttgtcag cttaacactt 60
aatatagtta aaaaagtcaa caattacctg caaaattata tataatntnaa tgtctaaaaa 120
tatgtngctt atatagagca ggaaaatccc tcctctccac aagggaagt ttcgttggtt 180
tncccagagc tgtgattatn gcagtactgt tacacgcatt tccaaagcat taaagancata 240
aatggggatta tctttncocct gcttgtgtat gcctgtnaaa taactgtacc agtggctttg 300
ctttctcata ggtcagtgac ttaaacagcc ctgtttcctt ttcggctata g ggcat 356

```

&lt;210&gt; 294

&lt;211&gt; 465

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(465)

<223> 5' terminal sequence. friend leukemia virus  
integration 1 (FLI1) gene.

&lt;400&gt; 294

```

gaccaaagca gtttcttgtc aatacacggg gttcagtatg acacagaatc atggacttaa 60
cccgcatgt tctggtttga gatttagtga caaatagagg tgggaagctt ataactaat 120
tttaggagga ccaaattcag tggatggcaa ctggaacatt gattgtaagg ccagtgaagt 180
tttcacccaa ctggaatttg atggaaagaa gggt tgtgtg ttttaagacgc caagggcatt 240
gcagaatccc tctcagtgga cagtatgcac tcagctgacc actctctcta gccaatagtc 300
aagatatgga actaaggaaa ttttaatgcc aaattacata cattcctgaa agacggggga 360
attaattna ctaattttnt tttttttttt ttaaagtatn gacagtggnt ccccggaact 420
tgggaaangt tgtaggggnt ttctaaacc aagncgattc gcant 465

```

&lt;210&gt; 295

&lt;211&gt; 2957

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2957)

<223> friend leukemia virus integrati on 1 (FLI1)  
gene.

&lt;400&gt; 295

```

gaattcccaa acgtgcacag gggagtgagg gcagggcgct cgcagggggc acgcaggag 60
ggcccagggc gccaggagg cgcgcgggg ctaatccgaa ggggctgcga ggtcaggctg 120
taaccgggtc aatgtgtgga atattgggg gctcggctgc agacttggcc aatggacgg 180
gactattaag gaggctctgt cggtgggtgag cgacgaccag tccctcttg actcagcgt 240
cggagcggca gccatctcc ccaaggcga catgactgcc tcggggagtc ctgactacgg 300
gcagccccac aagatcaacc ccctccacc acagcaggag tggatcaatc agccagtgag 360
ggtcaacgtc aagcgggagt atgaccacat gaatgatcc agggagtctc c ggtggactg 420

```



192/292

```

cagcgtagc aaatgcagca agctggtggg cggaggcgag tccaacccca tgaactacaa 480
cagctatagc gacgagaaga atggccccc tctcccaac atgaccacca acgagaggag 540
agtcacgtgc cccgcagacc ccacactgtg gacacaggag catgtgaggc aatggctgga 600
gtgggccata aaggagtaca gcttgatgga gatcgacaca tctttttcc agaacatgga 660
tggcaaggaa ctgtgtaaaa tgaacaagga ggacttcctc cgcgccacca ccctctacaa 720
cacggaagtg ctgtgtgcac acctcagtta cctcagggaa agttcactgc tggcctataa 780
tacaacctcc cacaccgacc aatcctcacg attgagtgtc aaagaagacc cttcttatga 840
ctcagtcaga agaggagctt ggggcaataa catgaattct ggctcaaca aaagtctctc 900
ccttgagggg gcacaaacga tcagtaagaa tacagagcaa cggccccagc cagatccgta 960
tcagatcctg ggcccagcca gcagtgcct agccaacct ggaagcgggc agatccagct 1020
gtggcaattc ctctggagc tgcctccga cagcgccaac gccagctgt a tcacctggga 1080
ggggaccaac ggggagttca aaatgacgga ccccgatgag gtggccaggc gctggggcga 1140
gcggaaaagc aagcccaaca tgaattacga caagctgagc cgggccctcc gttattacta 1200
tgataaaaac attatgacca aagtgcacgg caaaagatat gcttacaat ttgacttcca 1260
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cgtgccttca cacttaggca gctactacta gaagcttctt ctactgaag cccatcctgc 1560
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atggttaagt catggttctg agaaagaagc tgtacgtttt ctttatgttt ttatgaccaa 1860
agcagtttct tgtcaatata cggggttcag tatgacacag aatcatggac ttaaccgcgc 1920
atgttctggt ttgagattta gtgacaaata gaggtgggaa gcttataatc taattttagg 1980
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gaactaagaa attttaatgc aaatacatat attcctgaaa gacggggaat taaattacta 2220
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aaactcaagc agattcgcaa gtgctgtgcg cttgtcagac catcagacca gggccaacca 2340
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gttttactat cgaatcaatc gctgttattt ttttttaatg taatttgtac atcttttttc 2520
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cctatagctg aaaaggaaac agggctgtt aagtcactga cttatgagaa agcaaagcac 2640
tggtacagtt atttaacagg catacacaag cagggaaaag ataatccatt tagatcttta 2700
atgctttgga aatgcgtgta acagtactgc aataatcaca gctctgggaa aaacaacgaa 2760
actttccctt gtggagagga gggattttcc tgctctata t aagcaacata ttttagaca 2820
ttaaaatata tataattttg caggtaattg ttgacttttt taactatatt aagtgttaag 2880
ctgacaactg tcaaagaaga ccatgttgta aaataatttg actaaataaa tggttccttc 2940
tctcaaaaaa aaaaaaa 2957

```

&lt;210&gt; 296

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(400)

<223> 3' terminal sequence. ests, highly similar  
to tvhume hepatocyte growth factor receptor  
precursor [h.sapiens] (EST R97218) gene.

&lt;400&gt; 296

193/292

```

cacccttctt cttcacagat cacgaagatc ccattgaatg gcttgggctg cagacatttc 60
cagtcctgca gtcaatgcct ctctgcccc ccttttgttc agtgtggctg gtgcaganca 120
aatgtgtgcg atcggaggaa tgcctgagcg ggacatggac tcaacagatc tgtctgcctg 180
caatctacaa ggtaggaatc tctaacagct ggcatacatg tttttgtttg gtgttttttt 240
tttttttttg gtttggtttg gtttggtttt tgttttttta gatacaaatc ccactaatga 300
aaaaaattta aaaatcaatt tactcattta ggctgtgagg tcatcaggct aaagcaccat 360
ctctctcttg ggctttatcc ctggggcagg ggagggggg 400

```

&lt;210&gt; 297

&lt;211&gt; 464

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(464)

<223> 5' terminal sequence. ests, highly similar  
to tvhume hepatocyte growth factor receptor  
precursor [h.sapiens] (EST R97218) gene.

&lt;400&gt; 297

```

cgtgtagat tttcatagt cgaatatat gcttaagcaa ataaggcaac acagtttagca 60
tggctgcgat gttagccaat gtccattgcc agaaactgag ttctctatca gcaagagatg 120
tgctcatott gttctggact atatctctc a gggactaga gggcagcctg ctaaattggt 180
tgactcaat aaatatTTTT ggaatgaatt aaagagtggc atggcttaca gaagtataga 240
tgtagtata gtatccgtt gagcctttgc ttttttttct gggaacactg aaggaagact 300
cacagccacc catgggtgtt tgaccctcca ctgacctgc ccacctcacc ccgggaaata 360
atcttcagtc tcatctgttg aacagacaag gccacntct atggcttcgg nacaggtagn 420
aaaactgtcc tgtgtggccc cgctnggcag ggatcaccag tttg 464

```

&lt;210&gt; 298

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(378)

<223> 3' terminal sequence. ets variant gene 5  
(ets-related molecule) (ETV5) gene.

&lt;400&gt; 298

```

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aaacaatccc ccaaatcagg gcaaaacaaa atactgtcaa aagtgttaat cgcccttctc 120
ctaaataaaa agtcatccac actcagccac gtgattggga agagaaaggg ggcttgctct 180
acttgccgac cacatggccg ggtggttccc aagagtagcc atggtttatg attttgagaa 240
ccacggaggg ggnaaacagc tgttctgact gcccccitt ttctagacaa ggggtaatat 300
ttcagattca gctagaagag ctttccaat g ttttaagatg atttttaanc cttaatggtt 360
tnaggcctcc ccaacttt 378

```

&lt;210&gt; 299

&lt;211&gt; 317

194/292

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(317)

<223> 5' terminal sequence. ets variant gene 5  
(ets-related molecule) (ETV5) gene.

&lt;400&gt; 299

```
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caagctgagc cgctctctcc gctattacta tgaaaagggc atcatgcaga aggtggctgg 120
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ggataaccag cgtccgttcc tgaaggcaga gtccgagtgc cacctcagcg aggaggacac 240
cctgccgctg acccactttg aagacagccc cgcttacctc ctggacatgg accgctgcag 300
cagcctcccc tatgccg                                     317
```

&lt;210&gt; 300

&lt;211&gt; 4071

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4071)

<223> ets variant gene 5 (ets -related molecule)  
(ETV5) gene.

&lt;400&gt; 300

```
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tcgcccaggc gccagggccc gctgcgcgcg tgcgtgagcg cgcctgcgcc gccagggccg 120
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```

195/292

```

ccgctattac tatgaaaagg gcatcatg ca gaaggtggct ggagagcgat acgtctacaa 1560
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gctgcgttat attctgtact gtgtacaata aagaagtttg cttttcgttt a 4071

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&lt;210&gt; 301

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(407)

<223> 3' terminal sequence. cyclin-dependent  
kinase 4 (CDK4) gene.

&lt;400&gt; 301

```

nccngtataa aaaaggaccc caaatataaa ggtagggaaa gggacaagag ggaacata cc 60

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196/292

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ccttagtgta gagaaatggg aaggagaagg agaagcctca aaaggngagg tgggagggga 120
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cagagntaaa ggcaaagntt gccctctcag tntcngaag ggaaatggca gcttttcttc 240
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gggtgctgca gagctcgaaa ggcagagat tcgcttntgt ggggttaaaa gtcagccttt 360
nccgcagca gctttgcttc cccgactcct nccttttcag gnacccc 407

```

&lt;210&gt; 302

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(405)

<223> 5' terminal sequence. cyclin -dependent  
kinase 4 (CDK4) gene.

&lt;400&gt; 302

```

attcgnaca gaggaggagg tggaggaggc cttcccatca gcacagttcg tgaggtggct 60
ttactgaggc gactggaggc ttttgagca t cccaatgttg tccggctgat ggacgtctgt 120
gccacatccc gaactgaccg ggagatcaag gtaaccctgg tgtttgagca tgtagaccag 180
gacctaaaga catatctgga caaggcacc ccaccaggct tgccagccga aacgatcaag 240
gatctgatgc gccagtttct aagaggccta gatttccttc atgccaattg catcggtcac 300
cgaggatctg aagccagaga acattctggg tgacaagtgg ttggancagt caagctggct 360
ggactttggg cctgggcagn aatctancag cttaccagat gggca 405

```

&lt;210&gt; 303

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(420)

<223> 3' terminal sequence. v -yes-1 yamaguchi  
sarcoma viral oncogene homolog 1 (YES1) gene.

&lt;400&gt; 303

```

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ttaagtttag gctaccatta ttcatttaaa aaagtgtgct agaaggctgt ttttgccaac 120
ttcctttttt ggtaagggtt aacttcaca ttaagacact gaagacgaaa agctgttggt 180
aaaatatctc caaatattaca aagttgtttt tcttgggcaa tttaaaaata cagganfaat 240
ttaaantgaa tacacattaa ggtaggtgt tttatcccta ctatacaatt gttattatat 300
agggaaactgc tcccttcn gg ttaanccct aatggaatac ccatcaactt ttcccgccc 360
ntactttccc nggattgggg tttagggtac ctaaacggga aatttaggtc nccccnttg 420

```

&lt;210&gt; 304

&lt;211&gt; 4517

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4517)

<223> v-yes-1 yamaguchi sarcoma viral oncogene  
homolog 1 (YES1) gene.

&lt;400&gt; 304

```
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gtcgccctatc ctgaccacag caaagcggcc cggagcccg cggaggggacc tgacgggggc 120
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198/292

```

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```

&lt;210&gt; 305

&lt;211&gt; 459

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(459)

<223> 3' terminal sequence. interferon -induced  
protein 75, 52kd (IFI75) gene.

&lt;400&gt; 305

```

ncttgtctga aggtgtgctg gacacctcct ggggctcttc tgggtcattt ggttctggag 60
aattatctct tatctctggc atagagccca agggagagtg gggcatctct tgagggtctt 120
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gcncaatngg gtatggaagg aagcttcctt ctaanaagg 459

```

&lt;210&gt; 306

&lt;211&gt; 370

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

199/292

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(370)

<223> 5' terminal sequence. interferon -induced  
protein 75, 52kd (IFI75) gene.

&lt;400&gt; 306

```
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agacaactcc atcatcacta agagaatgta catggaatct ctggaagcct gtagaaattt 300
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ctgtntctctt                                     370
```

&lt;210&gt; 307

&lt;211&gt; 1541

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1541)

<223> interferon-induced protein 75, 52kd (IFI75)  
gene.

&lt;400&gt; 307

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tgaacagctt ggttgagtcg cccagcccat ctgaccctgt cctgcctctc cctgcactca 120
tccaggaagg aagaagcact tcagtgaacca atgacaagtt aacatccaaa atgaatgcgg 180
aagaagactc agaagagatg cccagcctcc tcaactagcac tgtgcaagtg gccagtgaac 240
acctgatccc ccaaataaga gataaagaag acctcaaga gatgcccac tctcccttgg 300
gctctatgcc agagataaga gataattctc cagaacccaa t gacccagaa gagccccagg 360
aggtgtccag cacaccttca gacaagaaag gaaagaaaag aaaaagatgt atctggtcaa 420
ctccaaaaag gagacataag aaaaaagcc tcccaagagg gacagcctca tctagacacg 480
gaatccaaaa gaagctcaaa aggttgatc aggttcctca aaagaaagat gactcaactt 540
gtaactccac ggtagagaca agggcccaaa aggcgagaaac tgaatgtgcc cgaaagtcga 600
gatcagagga gatcattgat ggcacttcag aaatgaatga aggaaagagg tcccagaaga 660
cgcttagtac accacgaagg gtcacacaag gggcagcctc acctgggcat ggcattccaag 720
agaagctcca agtggtggat aaggtgactc aaaggaaaaga cgactcaacc tggaactcag 780
aggtcatgat gaggttccaa aaggcaagaa ctaaattgtc ccgaaagtcc agatcgaaag 840
aaaagaaaaa ggagaaagat atctgttcaa gctcaaaaag gagatttcag aaaaatatcc 900
accgaagagg aaaaacccaaa agtgacactg tggattttca ctgttctaag ctccccgtga 960
cctgtggtga ggcgaaaggg attttatata agaagaaaat gaaacacgga tcctcagtga 1020
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atttaatttt cgagattacg gtgagccttt caggaagcaa tgtggttga cctggttaag 1500
ggaaaggctg attacggaaa tgtacacggt ggcccgaat t 1541
```

&lt;210&gt; 308

&lt;211&gt; 416

&lt;212&gt; DNA



200/292

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(416)

<223> 3' terminal sequence. v-myb avian  
myeloblastosis viral oncogene homolog -like 2  
(MYBL2) gene.

&lt;400&gt; 308

```
gttannncnan tnnatttttt aagagagagg caattttatt cttccaaaaa aatgcaccag 60
agagggtgag cacaggagca cccctggcca catcccccat cctaagcagg gtctgagatg 120
aggccaggnc tgacgtgggc ttgggagaag ctgacggagc tccctgtggc cttggggagg 180
gaaccaggca gacctgggaa gtggaacttt gttgttagca ccaggagccg cccacagctg 240
ggcttcggca acagggcagc acatggccct gtcccttcca cctgagagt c tggggagggg 300
ctggtggcag aaggctccct gcaggagggt cacctgaatg actctcagat tcacagaccc 360
cctnttgccc ccacaacccc tgtaaacatg agaatggggc tcgtgacacc ctnaac 416
```

&lt;210&gt; 309

&lt;211&gt; 426

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(426)

<223> 5' terminal sequence. v-myb avian  
myeloblastosis viral oncogene homolog -like 2  
(MYBL2) gene.

&lt;400&gt; 309

```
gaactcatca tcgaggacga catcaggccc gagaagcaga agaggaagcc tgggctgcgg 60
cggacccatt caagaaagtc cgaaggtctc tggctcttga cattgtggat gaggatatga 120
agctgatgat gtccacactg ccaaggtctc tatccttgcc gacaactgcc ccttcaaact 180
cttcagcct caccctgtca ggtatcaaag aagacaacag cttgctcaac cagggtttct 240
tgcaggccaa gcccgagaag gcagcagtgg ccagaagcc ccgaagc cac ttcacgacac 300
ctgcccttat gtccagtgcc tgggaagacg gtggcctgcg gggggaccag gggaccagct 360
tttcatggca ggagaaagcc cggcagcttc tggggccgct tgaagcccag ccacactttt 420
cgggac 426
```

&lt;210&gt; 310

&lt;211&gt; 2627

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2627)

<223> v-myb avian myeloblastosis viral oncogene  
homolog-like 2 (MYBL2) gene.

<400> 310  
gctgacgcct tgcagcgcgg ccc gggggccc ggagcggccg gagcagcccg ggtcctgacc 60  
ccggcccggc tcccgtcccg ggctctgcgg gcgggcgggc gagcgcggcg cggtcggggc 120  
cggggggatg tctcggcgga cgcgtgcga ggatctggat gagctgcact accaggacac 180  
agattcagat gtgccggagc agagggatag caagtgaag gtcaaatgga cccatgagga 240  
ggacgagcag ctgaggggccc tgggtaggca gtttgacag caggactgga agttcctggc 300  
cagccacttc cctaaccgca ctgaccagca atgccagtac aggtggctga gagttttgaa 360  
tccagacctt gtcaaggggc catggaccaa agaggaagac caaaaagtca tcgagctggt 420  
taagaagtat ggcacaaagc agtggacact gattgccaag cacc tgaagg gcgggctggg 480  
gaagcagtgc cgtgaacgct ggcacaacca cctcaaccct gaggtgaaga agtcttgctg 540  
gaccgaggag gaggaccgca tcatctgcga ggcccacaag gtgctgggca accgctgggc 600  
cgagatcgcc aagatgttgc cagggaggac agacaatgct gtgaagaatc actggaactc 660  
taccatcaaa aggaagggtg ac acaggagg cttcttgagc gagtccaaag actgcaagcc 720  
cccagtgtac ttgctgctgg agctcgagga caaggacggc ctccagagtg cccagcccac 780  
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tacagatctg gacgcagtgc gaacaccaga gcccttgagg gaattcccga agcgtgagga 960  
ccaggaaggc tccccaccag aaacgagcct gccttacaag tgggtgggtg aggcagctaa 1020  
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cctcacgccc aagagcacac ctgttaagac cctgcccttc tcgccctccc agtttctgaa 1500  
cttctggaac aaacaggaca cattggagct ggagagcccc tcgctgacat ccac cccagt 1560  
gtgcagccag aagggtggtg taccacacc actgcaccgg gacaagacac ccctgcacca 1620  
gaaacatgct gcgtttgtaa ccccagatca gaagtactcc atggacaaca ctccccacac 1680  
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catcaggagc gacatcaggc ccgagaagca gaagaggaag cctgggctgc ggcggagccc 1860  
catcaagaaa gtccggaaat ctctgctct tgacattgtg gatgaggatg tgaagctgat 1920  
gatgtccaca ctgcccagat ctctatcctt gccgacaact gcccttcaa actottccag 1980  
cctcacctg tcaggtatca aagaagaca cagcttgctc aaccagggct tcttgaggc 2040  
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tatgtccagt gcctggaaga cgggtggcct cgggggggacc agggaccagc ttttcatgca 2160  
ggagaaagcc cggcagctcc tgggcccgt gaagcccagc ca cacatctc ggaccctcat 2220  
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gcagaggggg tctgtgaatc tgagagtcac tcaggtgacc tcctgcagg agccttctgc 2340  
caccagcccc tccccagact ctacgttga ggcaacagg ccattgtgct ccctgttgcc 2400  
gagcccagct gtgggctg cctggtgcta acaacaaagt tccacttcca ggtctgcctg 2460  
gttccctccc caaggccaca gggagctccg tcagcttctc ccaagccac gtcaggcctg 2520  
gcctcatctc agacctgct taggatggg gatgtggcca ggggtgctcc tgtgctcacc 2580  
ctctcttggt gcattttttt ggaagaataa aattgcctct ctctttg 2627

<210> 311

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(442)

<223> 3' terminal sequence. transforming growth  
factor, beta receptor iii (betaglyc an, 300kd)

202/292

(TGFB3) gene.

&lt;400&gt; 311

```
cccagactca aggagttggt aaagggtaa tagccagata gtagaaccag tgaggagatg 60
cggccaaaga ttctttatat ctgaaccaag atgtaaaaca agaatgctt tgaggctttc 120
taagcgatcc tctgtctaa ttgacactt tgtctggatg cacacttctg accttgctgc 180
cacaacctgt ggggttctga tgtgtccctt gatgggtgct gccctcaggg actgcaccct 240
gacaagtgtt aaggcaacat tcttttctt tgcccggggc caaaaccaat gctgatgacc 300
ttatcagctt cctgtttctt cccatacttg catacaccac tggcaaaatg tcttaatggc 360
aaattttgta tttcttacag ggnctacagg aaatttgaaa atgg accaaa ttcagggaac 420
cacaggtttt gtggccatt tc 442
```

&lt;210&gt; 312

&lt;211&gt; 315

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(315)

<223> 5' terminal sequence. transforming growth  
factor, beta receptor iii (betaglycan, 300kd)  
(TGFB3) gene.

&lt;400&gt; 312

```
taacaaggag gtatcactga gcttatttta gctgcaaagt ggcatcatat tattccattt 60
aatgaaattc acctcaagcc ctttttgaca tattaatat atgggatata tttaa ggcaa 120
gagaagtaag gcaatccaaa tgagtgcctt ttccaatct cagcactgtc ttggnggaat 180
tggtgacact attcagataa ccaactggag accgacagat ttgccatgca tttgcatctt 240
gctagagttt ggtttttatg aaagggccta ttttttttta agttgacata ttttgagtgg 300
gaaacactca cccta 315
```

&lt;210&gt; 313

&lt;211&gt; 4208

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4208)

<223> transforming growth factor, beta receptor  
iii (betaglycan, 300kd) (TGFB3) gene.

&lt;400&gt; 313

```
tctttaagat ttgtagctac taagaaagaa aggagctttt tttccttggg cttcaaaact 60
gaaagaaccg catgagcctg acggcgcatg gtcttaacat caggctgtgc aggaagaagc 120
tatctgcaga tggatgccag cacacacaag gaagcagagc tctggcaaca ttgagtcaaa 180
gcaaggacac aacatcagag ggacggcaga gaatccttgt gtgtagtctt tgggtggcagt 240
ttgaaaattg caaggaggga cttaagact acttctgatt tgcaaagatg gtctgtgctc 300
cgagcaggct aaagtgactg gacgagacgc actgttgagg aaataaaaat gacttcccat 360
tatgtgattg ccattcttgc cctgatgagc ttctgttttag cca ctgcagg tccagagcct 420
ggtgcaactgt gtgaactgtc acctgtcagt gcctcccatc ctgtccaggc cttgatggag 480
agcttcactg ttttgtcagg ctgtgccagg agaggcaca ctgggctgcc acaggaggtg 540
```

203/292

```

catgtcctga atctcgcaact gcgccagggg cctggccagc tacagagaga ggtcacactt 600
cacctgaatc ccatctcctc a gtccacatc caccacaagt ctgttgtgtt cctgctcaac 660
tccccacacc ccctgggtgtg gcatctgaag acagagagac ttgccactgg ggtctccaga 720
ctgttttttg tgtctgaggg ttctgtggtc cagttttcat cagcaaactt ctccttgaca 780
gcagaaacag aagaaaggaa cttcccccat ggaatgaac atctgttaaa ttgggcccga 840
aaagagtatg gagcagttac ttcatccacc gaactcaaga tagcaagaaa catttatatt 900
aaagtggggg aagatcaagt gttccctcca aagtgaaca tagggaagaa ttttctctca 960
ctcaattacc ttgtgtagta cttcaaccc aaagcagcag aagggtgtgt gatgtccagc 1020
cagcccaga atgaggaagt acacatcatc gagctaata ccccaactc taaccctac 1080
agtgttttcc aggtggatat aacaattgat ataagacct ctcaagagga tcttgaagtg 1140
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tttgatgtta agggaagcct gaaaattatt gtcctaaca gtattggctt tggaaaagag 1260
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cagaaccgcg ccatccgggg aggggaaggc caaatggag gccttcctgt tcttttcca 1560
gatatttcca ggagagtctg gaatgaagag ggagaagatg ggctccctcg gccaaaggac 1620
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tacatctatt ctcacacagg ggagacagca ggaaggcagc aagtccccac ctccccgcca 2820
gcctcggaac acagcagtcg tgcccacagc atcgggcagca cgcagagcac gccttgctcc 2880
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ttcaccaccac acccagggtc agtataaaca tgaccctggg cttctgtacc acactagaat 3120
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agtgtcacca attccaccaa gacagtgtgt agattggaaa gggcactcat ttggattgcc 4080
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```

204/292

tccttggt

4208

&lt;210&gt; 314

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(468)

<223> 3' terminal sequence. peroxiredoxin 2  
(PRDX2) gene.

&lt;400&gt; 314

```
tnnttttttt tttncacctt tccctaatac ttnatnggtn acctctaggc ctgtgtgagg 60
ctgggtgggc ttgggggagg gcgtcactat tcagcttcta ggtggaggca tgagaaggcc 120
ttggctaggc cctccagggt cccatactgt ggagtttgga ggggcaggtc tggcctttcc 180
tggttcagca tagggcaccc aggtgggggn acaggtggac acccagcaca ggcacctagg 240
caggggcaca agctcantat ccnttagcca gcctaattgt ntttgg agaa atattccttg 300
ctgtcatcca cgttgggttt aatcgtgtca ctgccagggt tccagccagc gggacaaant 360
ttccccatgt tcgtttgtgt attgggaagg cctgggacca gccgcagagt tnatcccacg 420
gagngtccca aaggnaaatc attaaacagt gattttggcn aaggaaaa 468
```

&lt;210&gt; 315

&lt;211&gt; 394

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(394)

<223> 5' terminal sequence. peroxiredoxin 2  
(PRDX2) gene.

&lt;400&gt; 315

```
acttcaaggc cacagcgggt gttgatggcg ctttcaaaga ggtga agctg tcggactaca 60
aagggaagta cgtggctctc tttttctacc ctctggactt cactttttgtg tgccccaccg 120
agatcatcgc gttcagcaac cgtgcagagg acttccgcaa gctgggctgt gaagtgtctg 180
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ggaggcttgg gccccctgaa catc cccctg cttgctgacg tgaccagacg cttgtctgag 300
gattacggcg tgctgaaaac agatgagggc attgctaaca ggggcctctt tatcatcgat 360
gggcaagggt gttcctttcg ccagatcaat gta 394
```

&lt;210&gt; 316

&lt;211&gt; 937

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

205/292

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(937)

&lt;223&gt; peroxiredoxin 2 (PRDX2) gene.

&lt;400&gt; 316

```
cgcgccccca gggctcactt ggcgctgaga acgcggtgac agcgtgtgat cgtccgtgcg 60
tctagccttt gccacgcag ctttcagtca tggcctccgg taacgcg cgc atcggaagc 120
cagccctga cttcaaggcc acagcggtgg ttgatggcgc cttcaaagag gtgaagctgt 180
cggactacaa agggaaagta gtggtcctct ttttctaccc tctggacttc acttttgtgt 240
gccccaccga gatcatcgcg ttcacaaccg tgaagaggac ttccgcaaag ctgggctgtg 300
aagtgtctgg cgtctcgttg gactc tcaat tccccacct ggcttggatc aacaccccc 360
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tttgtccggc tgcttgaag cctggacgtg acacgattaa gccgaacgtg gatgacagca 660
aggaatatat ctccaaacac aattaggctg gctaaccgat agtgagcttg tgcccctgcc 720
taggtgcctg tgctgggtgt ccacctgtgc cccacctgg gtgcc ctatg ctgaccagg 780
aaaggccaga cctgcccctc caaaatccac agtatgggac cctggagggc tagcaaggcc 840
ttctcatgcc tccacctaga agctgaatag tgacgccctc cccaagccc accagccgc 900
acacaggcct agaggttaac aataaagtat tagggcc 937
```

&lt;210&gt; 317

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(451)

<223> 5' terminal sequence. v-fos fbj murine  
osteosarcoma viral oncogene homolog (FOS) gene.

&lt;400&gt; 317

```
gctagcacca tgagctgaag accgagccct ttgatgactt cctgttccca gcatcatcca 60
ggcccagtgg ctctgagaca gcccgctccg tggcagacat ggacctatct gggtccttct 120
atgcagcaga ctgggagcct ctgcacagtg gctccctggg gatggggccc atggcacagn 180
agctggagcc cctgtgcact ccggtgggtc cctgtactcc cagctgcact gctta cacgt 240
cttcttctgt cttcacctac cccgaggtg actncttccc cagctgtgca gctgcccacc 300
gcaaggcagc agcagcaatg agccttctc tgactcgttc agctnaccca cgggtgctggc 360
cctgtgaggg ggcaggggaa ggggaggcag ncggcaacna caagttgcca ttgtccgagt 420
tngttgattt anagagagga gaaacaaatt t 451
```

&lt;210&gt; 318

&lt;211&gt; 2084

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2084)

<223> v-fos fbj murine osteosarcoma viral oncogene  
homolog (FOS) gene.

&lt;400&gt; 318

```

aaccgcatct gcagcgagca actgagaagc caagactgag cggcgcgccg cggcgcgagcg 60
aacgagcagt gaccgtgtct ctacccagct ctgcttcaca gcgcccacct gtctccgccc 120
ctcgggccct cgcccggctt tgcctaaccg ccacgatgat gttctcgggc ttcaacgcag 180
actacgaggc gtcctcctcc cgctgcagca gcgcgtcccc ggccggggat agcctctctt 240
actaccaact acccgagac tccttctcca gcatgggctc gctgtcaac gcgcaggact 300
tctgcacgga cctggccgtc tccagtgcc aattcattcc cagggtcact gccatctcga 360
ccagtcgga cctgcagtgg ctggtgcagc ccgcccctgt ctctctgtg gcccctc gc 420
agaccagagc ccctaccct ttcgaggtcc ccgcccctc cgtggggct tactccaggg 480
ctggcgttgt gaagaccatg acaggaggcc gagcgagag cattggcagg aggggcaagg 540
tggaacagtt atctccagaa gaagaagaga aaaggagaat ccgaagggaa aggaataaga 600
tggctgcagc caaatgccgc aaccggagga gggagc tgac tgatacactc caagcggaga 660
cagaccaact agaagatgag aagtctgctt tgcagaccga gattgccaac ctgctgaagg 720
agaaggaaaa actagagttc atcctggcag ctacccgacc tgctgcaag atccctgatg 780
acctgggctt ccagaagag atgtctgtg cttcccttga tctgactggg ggcctgccag 840
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ccaagccctc agtgaacct gtcaagagca tcagcagcat ggagctgaag accgagccct 960
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ctgattagaa atgaccaata ttatactaag aaaagatacg actttatttt ctggtagata 1800
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gttactgata atgcattggt gagggtgtct gaattgtctg acattaacag ttttccatga 1920
aaacgtttta ttgtgttt tt aatttattta ttaagatgga ttctcagata tttatatttt 1980
tattttattt ttttctacct tgaggtcttt tgacatgtgg aaagtgaatt tgaatgaaaa 2040
atthaagcat tgtttgctta ttgttccaag acattgtcaa taaa 2084

```

&lt;210&gt; 319

&lt;211&gt; 240

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(240)

<223> 3' terminal sequence. retinoblastoma -binding  
protein 7 (RBBP7) gene.

&lt;400&gt; 319

```

ctgcaaaagc aatcaagaag tgttgaagg aaaaagtgtg aaagttatct ttgcataatt 60
gggaacagca agcacttagt ttgagaaaat gaggacttaa aacagttgan tcaaaggcaa 120
taccctgcta cttgtattta aaatcaatgg tgatgttatt tcttangca cattcttctc 180
ttccctaata gctacaant gatacagtac gcaacagctc acttgaaagt gctagantca 240

```

&lt;210&gt; 320

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<211> 457  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:primer  
  
<220>  
<221> misc\_feature  
<222> (1)..(457)  
<223> 5' terminal sequence. retinoblastoma -binding  
protein 7 (RBBP7) gene.

<400> 320  
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agaatacacc gtttctatat gacctgggta tgacccatgc ttttcagtgg cccagtctta 120  
ccgttcagtg gcttcttgaa gtgactaaac ctgaaggaaa agattatgcc cttcattggc 180  
tagtgctggg gactcatacg tctgatgagc agaatcatct ggtggttgct cgagtacata 240  
ttcccaatga tgatgcacag tttgat gctt cccattgtga cagtgacaag ggtgaatttg 300  
gtggcttttg ttctgtaaca gnaaaaattg aatgtgaaat taaaatcaat tcacgaagga 360  
gaagttaaac cgtgctogtt aacatggccg cagantcctt cacatccatt gcttacaaan 420  
acaccctctt gcttgatggg gttggnnttt tgactat 457

<210> 321  
<211> 1946  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer  
  
<220>  
<221> misc\_feature  
<222> (1)..(1946)  
<223> retinoblastoma -binding protein 7 (RBBP7)  
gene.

<400> 321  
gcctcgtag ctgcctgggc gggc tgggag gcgcggggtg aaaagtctcg ttccaagttt 60  
ggagagagag agaagagcgc ctgagacctc ggtacccgcg agcggggagg aggcaggaaa 120  
gaaggacgcg gcgtctgggg agcaccagc cagcaagacg gggcccgggc tttcgacagt 180  
ggggagtgtg acgcgcttgg gaaaggcagg agcgcagcgc gtcgggctgc tcttggttaa 240  
cgagaggagt ccgagggcgc ggcgaggggc gaacgaccgc acgcaagatg gcgagtaaag 300  
agatgtttga agatactgtg gaggagcgtg tcatcaatga agaataaaa atctggaaga 360  
agaatacacc gtttctatat gacctgggta tgacccatgc ttttcagtgg cccagtctta 420  
ccgttcagtg gcttcttgaa gtgactaaac ctgaaggaaa agatt atgcc cttcattggc 480  
tagtgctggg gactcatacg tctgatgagc agaatcatct ggtggttgct cgagtacata 540  
ttcccaatga tgatgcacag tttgatgctt cccattgtga cagtgacaag ggtgaatttg 600  
gtggcttttg ttctgtaaca ggaaaaattg aatgtgaaat taaaatcaat cacgaaggag 660  
aagtaaaccg tgctcgttac atg ccgcaga atcctcacat cattgctaca aaaacaccat 720  
cttctgatgt gttggttttt gactatacaa aacacctgc taaaccagac ccaagtggag 780  
aatgtaatcc tgatctcaga ttaagaggtc accagaagga aggctatggt ctctcctgga 840  
attcaaattt gaggggacat ctctaaagtg catctgatga ccatactgtt tgtctgtggg 900  
atataaacgc aggacaaaaa gaaggcaaaa ttgtggatgc taaaagccatc ttactggcc 960  
actcagctgt ttagaggat gtggcctggc acctgctgca cgagtcattg tttggatctg 1020  
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gtcacttggg ggatgcgcac actgccgaag tcaactgcct c tcattcaat ccctacagcg 1140  
aatattttct agccaccggc tctgcggata agaccgtagc tttatgggat ctgcgtaact 1200  
taaaattaaa actccatacc ttgcaatctc ataaagatga aattttccag gtccactggg 1260  
ctccacataa tgaaactatt ctggcttcaa gtggtactga ccgccgcctg aatgtgtggg 1320



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```
atttaagtaa aattggggaa gaacaatcag cagaagatgc agaagatggg cctccagaac 1380
tcctgtttat tcatggagga cacactgcta agatttcaga ttttagctgg aaccccaatg 1440
agccttgggt catttgctca gtgtctgagg ataacatcat gcagatatgg caaatggctg 1500
aaaatattta caatgatgaa gagtcagatg tcacgacatc cgaactggag ggaca aggat 1560
cttaaaccca aagtacgaga aatgtttctg ttgaatgtaa tgctacatga atgcttgatt 1620
tatcaagcgc caaaaaggca ttgtatagta ggaaatgtaa gtggggtggc ttatggcttc 1680
tttatcctct gattctagca cttcaagtg agctgttgcg tactgtatca tattgtagct 1740
attaggaag agaagaatgt tgcttaagaa agaacatcac cattgatttt aaatacaagt 1800
agcagggtat tgctttgat tcaactgttt taagtctca ttttctcaaa ctaagtgtt 1860
gctgttccca aatatgcaag aataactttt acactttttc cttccaacac ttcttgattg 1920
gctttgcaga aataaagttt taaaat 1946
```

&lt;210&gt; 322

&lt;211&gt; 365

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(365)

<223> 3' terminal sequence. kiaa1075 protein  
(KIAA1075) gene.

&lt;400&gt; 322

```
tatagaaatt ctttattatt agacaaaaat agactctctt ttttcccta ttcattgtat 60
cctactctga atctctgctc agaggaggca gtgactcgct cccaccct ctccatccc 120
tgccgtgctg gcacctgcag ctgggtggaa ctggcagggg ctgatcccct gggagggctg 180
acgttctcct gcaggtgggg ctgcctgac tccttcgggg ctcaactgct gatgcctcct 240
caccctcac acaccatct ctgccatctg ctacatggc aagggtcatc ttgtggggcc 300
tggtccactt taacttaggc agggctgggg ggcgggggaa gggagaggca gtgttcccag 360
gggcc 365
```

&lt;210&gt; 323

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(400)

<223> 5' terminal sequence. kiaa1075 protein  
(KIAA1075) gene.

&lt;400&gt; 323

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tcaagggttg cccagtgag ccctactttg gcagcctgtc cgccttggtc tcccagcact 60
ccatctcccc catctccctg cctgtctgcc tgcgcattcc cagcaaagat cctctggaag 120
agaccccaga ggtccagtg ccaccaaca tgagcacagc gncagacctc ctgcgtcagg 180
gtgtgcctg caggtngctc tacttgacct cagtggagac agagtactg acgggcccc 240
aagctgtggc ccgggccagc tctgcagctc tgagctgta g cccccgccg acaccagctg 300
ttgtccactt caaggtgtca gccaggga ttnacactga cgggacaacc aaaggaagct 360
cttnttttgc gccgccatta tccagtgga cagcatcacc 400
```

209/292

<210> 324  
<211> 489  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(489)  
<223> 5' terminal sequence. atp-binding cassette,  
sub-family c (cftr/mrp), member 5 (ABCC5) gene.

<400> 324  
nttcggcaca gnaagataca actctgtgct gaacagctgc tgcctgaggc tgacctggcc 60  
attcttccca gcagcgacct gacggagatt ggagagcgag tancaacctg agcgggtggc 120  
agcgcagagg atcagccttg cccgggcctt gtatagtgc aggagcatct acatcctgga 180  
cgaccccttc agtgcccttag atgcccattg ggaanccaca tncctcaata gtgctatccg 240  
gaaacatctc aagtccaaga cagttctgtt tgttaccac cagt tacagt acctgggttg 300  
actgtgatga agtgatcttc atgaaagagg gctgtattta cgggaaagag ggcacccntg 360  
gagggaantg atggatttta aatgggtgatt atggttacct ttttaattaa cntgtgtgtg 420  
ggggagagac accgccattg agntcatttc aaaaagggga accgtnggtt cacagaggag 480  
ttcacagtt 489

<210> 325  
<211> 5838  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(5838)  
<223> atp-binding cassette, sub-family c  
(cftr/mrp), member 5 (ABCC5) gene.

<400> 325  
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aggggcgcag gaattctgat gtgaaactaa cagtctgtga gccctggaac ctccgctcag 120  
agaagatgaa ggatatcgac ataggaaaag agtatatcat cccagtcct gggtagagaa 180  
gtgtgaggga gagaaccagc acttctggga cgcacagaga ccgtgaagat tccaagtcca 240  
ggagaactcg accgttgga tgccaagatg ccttggaac agcagcccga gccgagggcc 300  
tctctcttga tgcctccatg cattctcagc tcagaatcct ggatgaggag catccaagg 360  
gaaagtacca tcatggcttg agtgccttga agcccatccg ga ctacttcc aaacaccagc 420  
accagtgga caatgctggg cttttttcct gtatgacttt ttctgtggctt tcttctctgg 480  
cccgtgtggc ccacaagaag ggggagctct caatggaaga cgtgtggtct ctgtccaagc 540  
acgagtcttc tgacgtgaac tgagaagac tagagagact gtggcaagaa gagctgaatg 600  
aagttgggcc agacgctgct tccctgcgaa ggggtgtgtg gatcttctgc cgcaccaggc 660  
tcatcctgtc catcgtgtgc ctgatgatca cgcagctggc tggcttcagt ggaccagcct 720  
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gaggacccgt tgttgccatc ttaggcatga tttataatgt aattattctg ggaccaacag 1080  
gcttcctggg atcagctgtt tttatcctct tttaccagc aatgatgttt gcatcacggc 1140  
tcacagcata tttcaggaga aaatgcgtgg ccgccacgga tgaacgtgtc cagaagatga 1200

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```

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agggtatcac tgtgggtgtg gctcccattg tgggtgtgat tgccagcgtg gtgaccttct 1380
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taaagaacaa accagccagt cctcacatca agatagagat gaaaaatgcc accttggcat 1620
gggactcctc ccactccagt atccagaact cgcccaagct gaccccaaaa atgaaaaaag 1680
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ccctcatcg cgtctccta ccgaaacctt gccttctctg attttatctt tcgcacagca 4560
gttccggatt ggcttgtgtg tttcactttt agggagagtc atattttgat tattgtattt 4620
attccatatt catgtaaaaa aaatttagtt tttgttctta attgcactct aaaaggttca 4680
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tctatatata attctgtaca tagcctatat ttacagtga aatgtaagct gtttatttta 4800
tattaaaaata agcactgtgc taataacagt gcatattcct ttctatcatt tttgtacagt 4860

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211/292

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ttgctgtact agagatctgg ttttgctatt agactgtagg aagagtagca tttcattctt 4920
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caaaaatctg aaaatgtgaa taaaattatt ttggattttg taaaaaaaaa aaaaaaaaaa 5820
aaaaaaaaa aaaaaaaaaa                                     5838

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&lt;210&gt; 326

&lt;211&gt; 385

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(385)

<223> 3' terminal sequence. cadherin 1, type 1,  
e-cadherin (epithelial) (CDH1) gene.

&lt;400&gt; 326

```

aanganatat taacaaaatt gtttaataaa atttataaaa atgcatcttt gagaatactt 60
tnctcagctt gaattgtttt ctttttccac ccccaaagaa aatacacaat tatcagcacc 120
cacacatgta tacactcaaa actacagtga catt ctctac acagnnctat attogatata 180
gcttgaactg ccgaaaaatc angacaattc caaaagggtga ttgcagggtt gatttttttc 240
tccaaaacac ttgaganaca gtaaagctat ttcaacaaag gtcttttctt tgattgtcaa 300
aggttgaaat tcacatttna ntannagggg ntcnaatca ngntcctcac taccctctac 360
ccctcancta accccctttg gggcc                                     385

```

&lt;210&gt; 327

&lt;211&gt; 423

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(423)

<223> 5' terminal sequence. cadherin 1, type 1,  
e-cadherin (epithelial) (CDH1) gene.

&lt;400&gt; 327

```

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gtttgtgtct ttgtctggcc acatcttgac taggtattgt ctactctgaa gacctttaat 120
ggcttccctc tttcatctoc tgagtatgta acttgcaatg ggcagctatc c agtgacttg 180

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ttctgagtaa gtgtgttcat taatgtttat ttagctctga agcaagagt atatactcca 240  
gggacttaga atagtgccta aagtgtctga gccaaagaca gagcggaact atgaaaagt 300  
ggcttgagaga tggcaggaga gcttgtcatt gagcctgggc aatttnagca aactgatgtc 360  
tgaggatgat tgcaggtggg tcttacctca tctactgnaa aattctggta aggaatggga 420  
ggg 423

&lt;210&gt; 328

&lt;211&gt; 4828

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4828)

<223> cadherin 1, type 1, e-cadherin (epithelial)  
(CDH1) gene.

&lt;400&gt; 328

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gtccagccc ggcccagccc gaccgcaccc ggcgctgcc ctgcctcggc gtcccggcc 120  
agccatgggc ccttgagacc gcagcctctc ggcgctgtg ctgctgtgc aggtctctc 180  
ttggctctgc caggagccgg agccctgcc ccttggttt gacgccgaga gctacacgtt 240  
cacggtgccc cggcgccacc tggagagagg cgcgtcctg gccagagtga atttgaaga 300  
ttgcaccggg cgacaaagga cagcctatct tccctcgac acccgattca aagtgggcac 3 60  
agatggtgtg attacagtca aaaggcctct acggtttcat aaccacaga tccatttctt 420  
ggtctacgcc tgggactcca cctacagaaa gtttccacc aaagtcacgc tgaatacagt 480  
ggggcaccac caccgcccc cgccccatca ggctccgtt tctggaatcc aagcagaatt 540  
gtcacattt cccaactcct ctctgtgcct cagaagacag aagagagact gggttattcc 600  
tcccatcagc tgcccagaaa atgaaaaagg cccatttctt aaaaacctgg ttcagatcaa 660  
atccaacaaa gacaaagaag gcaaggtttt ctacagcatc actggccaag gagctgacac 720  
acccctgtt ggtgtcttta ttattgaaag agaaacagga tggctgaagg tgacagagcc 780  
tctggataga gaacgcat tg ccacatacac tctcttctct cagctgtgt catccaacgg 840  
gaatgcagtt gaggatccaa tggagatttt gatcacggta accgatcaga atgacaacaa 900  
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213/292

```

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gcctgaagtg actcgtaacg acgttgacac aacctcatg agtgtccccc ggtatcttcc 2520
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&lt;210&gt; 329

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(471)

<223> 5' terminal sequence. zinc finger protein  
144 (mel-18) (ZNF144) gene.

&lt;400&gt; 329

```

attcggcaca tgattccact tccgtttccc agggcaacgc tcccagtc cccaccc cc 60
gaccccgga tcatgcatcg gactacacgg atcaaaatca cagagctgaa cccacacctc 120

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214/292

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atgtgtgccc tctgcggggg gtacttcacg gacgccacca ctatcgtgga gtgcctgcat 180
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gacgtgcagg tccataaaac ccggccgctg ctgagca ttc aggtctgaca aaacatttca 300
agacattgtc ttacaaattg gtccctgggg ctttttaaag atggagattg aaacgggcgg 360
cgggatttct tatggcaggc gttacccctt ggacgggagg ttcccccaac ggnttccaat 420
tgaggggacc ngggcgaggg tttttnngga ggcagggaga aggggggttt t 471
```

&lt;210&gt; 330

&lt;211&gt; 2227

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2227)

<223> zinc finger protein 144 (mel -18) (ZNF144)  
gene.

&lt;400&gt; 330

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cagcctcttg tcccagagc ggactttgga agctgaactg cttttgttgc tggaagactt 120
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cccactcccg accccggaat catgcatcgg actacacgga tcaaaatcac agagctgaac 240
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tcacctgggg cctagagtgg aagtgggggt ggggttaacct cacacaagca cagatcccag 2160
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<210> 331  
<211> 254  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(254)  
<223> 3' terminal sequence. macrophage stimulating  
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 331  
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gacacgcgtg aagacagctg gccagcggga ccttgcgcat actcggttgg ggattataat 180  
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cacaggcccc caca 254

<210> 332  
<211> 362  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(362)  
<223> 5' terminal sequence. macrophage stimulating  
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 332  
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gaagtgtggc aagaggtgg atcggctgga tcagcggcgt tccaagctgc gctggttggg 180  
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tgcggnggt ctctagtga ggagcagtn atactgactn cccggaagtg cttctcctcc 300  
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ag 362

<210> 333  
<211> 2219  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2219)  
<223> macrophage stimulating 1 (hepatocyte growth  
factor-like) (MST1) gene.



&lt;400&gt; 333

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gctacatgcg gtggtgcccg ggccttggca ggagatgtg gcagatgctg aagagtgtgc 180
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agtccataat gtggccttct tgaatgttat ctccaaccag gagtgtaca tcaagcaccg 1920
aggacgtgtg cgggagagtg agatgtgcac tgagggactg ttggccctg tgggggcctg 1980
tgagggtgac tacgggggccc cacttgctg ctttaccac a actgctggg tcctggaagg 2040
aattataatc cccaaccgag tatgcgcaag gtcccgttg ccagctgtct tcacgcgtgt 2100
ctctgtgttt gtggactgga ttcacaaggc catgagactg ggtagggcc agccttgatg 2160
ccatatgcct tggggaggac aaaacttctt gtcagacata aagccatgtt tcctcttta 2219
```

&lt;210&gt; 334

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(431)

<223> 3' terminal sequence. glutathione  
s-transferase pi (GSTP1) gene.

&lt;400&gt; 334

```
gaaaggaagg caaactctgc ccccc gctca gagtcccccc aaccctcaact gtttcccggt 60
gccattgatg gggaggttca cgtactcagg ggaggccagg naggcntgna gcttggggccg 120
ggcactgagg cgcgccacat atgtgagag caggggggaa gcatccaggc agccagggt 180
agggaccnca tggatcagca gcaagtccag caggttntag tcagcgaagg agntctggtc 240
tcccacaatg aaggtcttgc ctccctggtt ctgggacagc aggttctcaa aaggcttcag 300
```

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ttgcccgggc agtgccttca catagtcac cttgcccgcc tcatagttgg tntagatgag 360  
ggagatgtat ttgcagcgga ggtcctccac gccgttcatt tcacctgtcc accagggctg 420  
nctcctttt t 431

&lt;210&gt; 335

&lt;211&gt; 305

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(305)

<223> 5' terminal sequence. glutathione  
s-transferase pi (GSTP1) gene.

&lt;400&gt; 335

nattcggcac aggtcgccac catgccgccc tacaccgtgg tctatttccc agttcgaggc 60  
cgctgcctgt cggcaatgct gctggcagat cagggccaga gctggaagga ggaggtngtg 120  
accgtggaga cgtggcagga gggctcactc aaagcctcct gcctatacgg gcagctcccc 180  
aagtccagg acggagacct naccctgtac cagt ccaata ccatcctgcg tcacctgggc 240  
cgcacccttg ggctnctatg ggaaggacca gcaggangca gccctggtgg acatngtgaa 300  
tgacg 305

&lt;210&gt; 336

&lt;211&gt; 737

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(737)

&lt;223&gt; glutathione s-transferase pi (GSTP1) gene.

&lt;400&gt; 336

ggagtttgcg cgccgcagtc ttgccacca tgccgccta caccgtggtc tatttcccag 60  
ttcgaggccg ctgcgcggcc ctgcgcatgc tgctggcaga tcagg gccag agctggaagg 120  
aggaggtggt gaccgtggag acgtggcagg agggctcact caaagcctcc tgcctatacg 180  
ggcagctccc caagttccag gacggagacc tcacctgta ccagtccaat accatcctgc 240  
gtcacctggg ccgcaccctt gggctctatg ggaaggacca gcaggaggca gccctggtgg 300  
acatggtgaa tgacggcgtg gag gacctcc gctgcaaata catctccctc atctacacca 360  
actatgaggc gggcaaggat gactatgtga aggcactgcc cgggcaactg aagccttttg 420  
agaccctgct gtcccagaac cagggaggca agaccttcat tgtgggagac cagatctcct 480  
tcgctgacta caacctgctg gacttgctgc tgatccatga ggtcctagcc cctggctgcc 540  
tgatgcgtt cccctgctc tcagcatatg tggggcgcc cagcgcccg cccaagctca 600  
aggccttcc ggcctcccct gagtacgtga acctcccat caatggcaac gggaaacagt 660  
gagggttggg gggactctga gcgggaggca gagtttgcct tcctttctcc aggaccaata 720  
aaatttctaa gagagct 737

&lt;210&gt; 337

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(372)

<223> 3' terminal sequence. b-cell cll/lymphoma 2  
(BCL2) gene.

&lt;400&gt; 337

```
gtgggnctgt gttgaaacag gccacgtaaa gcaactctct aaaggtcaaa ccaccataga 60
tttgaatctg ctgggtcattc gccatctgga tttttaactg aatgaatctc atgggtttta 120
ccaaacatgc atgtaatcct gaataccatg anttaaatgc gganttgccc agggacgagg 180
aaaccttcaa gaaacaaggt caaagggaca ncagatata a ctgtcacant aaacanttct 240
gttgacgtgg gaaatgcaca tgacttggtt gaaacaaagc tcctcagtgg gccagtgaca 300
tccnggggtt ttcttagggt aggctgagga ctgaggggt tatctcacct tctcaggaat 360
gctttttgaa gg 372
```

&lt;210&gt; 338

&lt;211&gt; 508

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(508)

<223> 5' terminal sequence. b-cell cll/lymphoma 2  
(BCL2) gene.

&lt;400&gt; 338

```
nttcggcaca gacttttttt aagctaccaa ttg tgccgag aaaagcattt tagcaattta 60
tacaatatca tccagtacct taaacctga ttgtgtatat tcatatattt tggatacgca 120
ccccccaact cccaatactg gctctgtctg agtaagaaac agaatcctct ggaacttgag 180
gaagtgaaca tttcggtgac ttccgcatca ggaaggctag agttaccag agcatcaggc 240
cgccacaagt gcctgctttt aggagaccga agtccgcaga acctgcctgt gtcccagctt 300
ggaggcctgg gtcctgggaa ctgagccggg gccctcactg gccttccttc caggggatgg 360
atcaacaggg gcagtggtgt cttccgaatg tctgggaagc tgatgggagc tcagantttc 420
cactgtcaag aaagaggcag ttaggagggg tttgggtggg gcttggtcac ctgg ggggcc 480
ttccaggtag ggcccttttt aagtggga 508
```

&lt;210&gt; 339

&lt;211&gt; 445

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(445)

<223> 3' terminal sequence. proliferating cell  
nuclear antigen (PCNA) gene.

&lt;400&gt; 339

219/292

```
tttttttant caaaagtttg aaattcaagt aactttatnt aaattcaaaa acaattctta 60
aaactgcatt tagagtcaag acccttttgt attataaaaa tcacaagtat ttctaagaga 120
caaaaatact tctaggttaa ctagaccaga tctgactt tg gactttattc tttaaacaan 180
ttgcagagan tagagaaaaa antaggttat ttacagaaaa caatatctac atatgtactt 240
ngnggtacaa ntttgggtga cagaaaagac ttcagggtata tgctgggcat cttaggaagn 300
cagttctcaa agggnccttag gttttatntn cttggatttt taaggattgc cctaagganc 360
ccttcttcat cctcgn tctt ggggngggc aggtaggtnt tttaggtgtc ccntatccc 420
ganttttata ctctncaccg ggggg 445
```

&lt;210&gt; 340

&lt;211&gt; 437

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(437)

<223> 5' terminal sequence. proliferating cell  
nuclear antigen (PCNA) gene.

&lt;400&gt; 340

```
gtccagcgt tgtaaacctg cagagatgga ctgctccac gtctcttttg tgcagctcac 60
cctgcggtct gagggtctcg acacctaccg ctgcgaccgc aacctggcca tggggtgaac 120
ctcaccagta gtcccaaat actaaaatgc gccggcaatg aagatatcat tacactaagg 180
gccgaagata acgcggatac cttggcgcta gtatttgaag caccaaacca ggagaaagt 240
tcagactatg aaatgaagtt gatggattta gatgttgaac aacttngaag tccagaacag 300
gagtacagct gtgtagtaaa gatgccntct ggtgaatttg c acgtatatg ccgagatctc 360
agccatattg ggagatgctg ttgtaatttc ctgtgncaaa agacgggagt gaaaattttt 420
ctgcaagtgg gagnact 437
```

&lt;210&gt; 341

&lt;211&gt; 1231

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1231)

<223> proliferating cell nuclear antigen (PCNA)  
gene.

&lt;400&gt; 341

```
aggtctcagc cggctcgtgc gacgttcgcc cgctcgtctt gaggtctcctg aagccgaaac 60
tagctagact ttcctccttc ccgcctgcct gtagcggcgt tggtgccact ccgccaccat 120
gttcgaggcg cgcctggtcc agggctccat cctcaagaag gtgttgagg cactcaagga 180
cctcatcaac gaggcctgct gggatattag ctccagcggg gtaaacctgc agagcatgga 240
ctogtcccac gtctcttttg tgcagctcac cctgcggtct gagggcttcg acacctaccg 300
ctgcgaccgc aacctggc ca tgggcgtgaa cctcaccagt atgtccaaaa tactaaaatg 360
cgccggcaat gaagatatca ttactaag ggccgaagat aacgcggata ccttggcgct 420
agtatttgaa gcacaaacc aggagaaagt ttcagactat gaaatgaagt tgatggattt 480
agatgttgaa caacttgaa ttccagaaca ggagtacagc tgtgtagtaa agatgccttc 540
tggtgaattt gcacgtatat gccgagatct cagccatatt ggagatgctg ttgtaatttc 600
ctgtgcaaaa gacggagtga aattttctgc aagtggagaa cttggaaatg gaaacattaa 660
```

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```

attgtcacag acaagtaatg tcgataaaga ggaggaagct gttaccatag agatgaatga 720
accagttcaa ctaacttttg cactgaggta cctgaact tc tttacaaaag ccactccact 780
ctcttcaacg gtgacactca gtatgtctgc agatgtaccc cttgttgtag agtataaaat 840
tgcggatatg ggacacttaa aatactactt ggctcccaag atcgaggatg aagaaggatc 900
ttaggcattc ttaaaattca agaaaataaa actaagctct ttgagaactg cttctaagat 960
gccagcatat actgaa gtct tttctgtcac caaatttgta cctctaagta catatgtaga 1020
tattgttttc tgtaaataac ctattttttt tctctattct ctccaatttg tttaaagaat 1080
aaagtccaaa gtctgatctg gtctagttaa cctagaagta tttttgtctc ttagaaatac 1140
ttgtgatttt tataatacaa aagggtcttg actctaaatg cagttttaag aagtg ttttt 1200
gaatttaaat aaagttactt gaatttcaaa c                                1231

```

&lt;210&gt; 342

&lt;211&gt; 383

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(383)

<223> 3' terminal sequence. adenovirus 5 ela  
binding protein (BS69) gene.

&lt;400&gt; 342

```

tttttttttt aaacacacan gttttcacgc tgtagtaact tggaaatgtg caaccctgtg 60
caacagagac agaaaagcca aagtaacacg aatctcactt tcatgcagct atcagttaaa 120
tattacatac tctggaatga ttttacacca aaaatattt c cacaattact tgctctcata 180
ggggtggatc gaagtcttaa aacttgaaaa acaatcaaag aaggttaagt gttctcgggt 240
ctgacatctc catcagcgcc acacactgtg gngaacactg gactaattac acagcaacaa 300
ggaggggaac gatgatgcca agttactgca taatttaggg tacattgtat ggaatggggg 360
gctactgggg gtactttttt tac                                383

```

&lt;210&gt; 343

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(483)

<223> 5' terminal sequence. adenovirus 5 ela  
binding protein (BS69) gene.

&lt;400&gt; 343

```

gttnaaattg cagggactgg ggtaatcttt tactgagctg gatcttagag aaaatgaata 60
tttaaatttt aaagtttgca catttcactt ttgtcctaac atgagtgtt gtaacaaaaat 120
aaacaacaaa aacaaagcca aaaactacct ttatccatat gtgaaattat agatgaggca 180
tacgaatttg ttaaatgctt cccttccctt occacatata atctcactgc ctattatctg 240
gtgtcacctc atgtatcgta agttaatact aaaagaagag aaagcactta agtttcacag 300
aagccgttat gttttagagt aatgggtgca ttgcctaagt gaactccatc actgtacaca 360
gaatgaagga nttaatgcca tgtaatttt cttgttattt aagg atgccg tggatttggt 420
aaaaggctct gtattttgcy gggatgtctg gggttaggga ggccttacc ataggggntg 480
ggg                                483

```

<210> 344  
<211> 2722  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2722)  
<223> adenovirus 5 ela binding protein (BS69)  
gene.

<400> 344  
ggagcataat gctaaagaag taaacaggtc atggcacggt taacaaaaag acgacaggcg 60  
atacaaaagc tatccagcat ctttgggcag ccattgagat tata cggaac cagaagcaga 120  
ttgccaaatc tgaccgtatt acaaaatgtg aaacaactac attattcttg aacctatggt 180  
gatttttaca tcattacaca gatatgtcat tttcattagt tgtatcattg ttataaaactg 240  
gtatgtgtct cgagtcacag gtatgcaccc taaagagacc acccgtcagc tgagcttagc 300  
tgtgaaaagat ggtcttattg tc gaaactct aacagtgggc tgcaaagggt caaaagctgg 360  
tattgaacaa gaaggatatt ggttgccagg agatgagatt gactgggaaa cagaaaaatca 420  
tgactggtat tgttttgaat gccatttgcc tggagagggt ttgatattgt acctgtgttt 480  
tcgtgtgtat cattccaagt gtttgtctga tgagttcagg cttagagaca gcagtagtcc 540  
ctggcaagtgc ccagtttgca ggagcattaa gaagaagaat acaaacaaac aggagatggg 600  
cacatacctc agattcattg tctcccgcat gaaggagagg gctatagatc ttaataaaaa 660  
ggggaaggac aataaacacc cgatgtacag gaggtggtg cactcagctg tggacgttcc 720  
caccattcaa gagaagtgat atgaaggga ataccgaagt ta tgaagagt tcaaagctga 780  
tgcccaattg cttctccaca ataccgtgat tttctatgga gcagacagtg agcaagctga 840  
cattgcgagg atgctatata aagacacatg tcatgagctg gatgaactgc agctttgcaa 900  
gaattgcttt tacttgtcaa atgctgtctc tgacaactgg ttctgttatc cttgtatacc 960  
taatcatgag ctggtttggg ctaaaatgaa aggttttggg ttttggccag ccaaagtcac 1020  
gcagaagaag gacaatcaag tcgacgttcg cttctttggc caccaccacc agagggcctg 1080  
gattccttct gaaaacattc aagatatcac agtcaacatt catcggtcgc acgtgaagcg 1140  
cagtatgggt tggaaaaagg cctgtgatga gctggagctg catcagcgtt tcctacgaga 1200  
aggagattt tggaaatcta agaagagga ccgagggtgag gaagaggcag aatccagtat 1260  
ctcctccacc agtaatgagc agctaaagg cactcaagaa ccaagagcaa agaaaggacg 1320  
acgtaatcaa agtgtggagc ccaaaaagga agaaccagag cctgaaacag aagcagtaag 1380  
ttctagccag gaaataccca cgatgcctca gccc atcgaa aaagtctccg tgtcaactca 1440  
gacaaagaag ttaagtgcct cttaccaag aatgctgcac cggagcacc agaccacaaa 1500  
cgacggcgtg tgtcagaca tgtgccatga caaatacacc aagatcttca atgacttcaa 1560  
agaccggatg aagtcggacc acaagcggga gacagagcgt gttgtccgag aagctctgga 1620  
gaagctgctg tctgaaatgg aagaagaaa gagacaagct gtaaataaag ctgtagccaa 1680  
catgcagggt gagatggaca gaaaatgtaa gcaagtaaag gaaaagtgtg aggaggaatt 1740  
tgtagaagaa atcaagaagc tggcaacaca gcacaagcaa ctgatttctc agaccaagaa 1800  
gaagcagtggt tgctacaact gtgaggagga ggccatgtac cactgctg ct ggaacacatc 1860  
ctactgctcc atcaagtgcc agcaggagca ctggcacgcg gagcacaagc gcacctgccg 1920  
ccggaaaaga tgaagctggc ccttcccgga gtcaccccga tgattactct tttcagacac 1980  
agcgggtttt gtttccaaga agccaaaatt gtttagaatt tgcttcccat tttgcaccag 2040  
cctttaaaca cttttcgtga ag aaattttg cacagtagtt taaatctttt gttaatgctc 2100  
ctccgaagtt tttcagggg taaaagtaac atcagtggag ggtattattt taaataaatt 2160  
ttaattgaga atttgttgca ttttcagcaa attttaaac atttttagggt tttacagaga 2220  
ttttaacctt taaacaacag atctttaaaa aacagggtgaa tacaagttag tttacaaaag 2 280  
aaacatttag aatgatatct aatgtaagaa ctacagaact gtttcagaaa taaaacatac 2340  
taccttgatg tgacattttt ttcttaacct gtgtgagctg gttttgttca gcttaattta 2400  
ctgttcaaag gcattatctg ttggtcacac cagtgggtat atgattgaat ttagggaaca 2460  
gggttgacac agcagggcta gtctgcata tttttt ctta aatatttccc aattgtgttt 2520  
ttcattatct cttttcaata tataactttt ataacaaatt attagctttg atctttagt 2580  
ttaaaattgc agggaactgg ggtaatcttt tactgagctg gatccttagag aaaatgaata 2640  
tttaaatatt aaagtttgcc acatttcac tttgtcctaa catgagtgtc tgtaacaaaa 2700

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taaaacaaca aaaacaaagc ct

2722

&lt;210&gt; 345

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(363)

&lt;223&gt; 3' terminal sequence. matrix

metalloproteinase 11 (stromelysin 3) (MMP11) gene.

&lt;400&gt; 345

```
gcattgcagca tcctgagtgg tagcgtgat ctacagagggc acccctctcc agtcagtggc 60
cctgcgggna cggngactgt ctacacgccg ggtgctgggg tggaaacgcc agtagtcctt 120
gcctcggaag aagtagatct tgttcttctc gggacccag accaaggc ag catggaccgg 180
gaacctcacc agggcccagc tcggtgaggg gtgcggggcc cagggactgg cttttcaccg 240
tcgtacaccc agtacttgag caccttgga agaaccaaat gtgggcccgg cttaccagc 300
attggccttt tcgccacagg gctggggcag tccctgccag tngcgagaag ccaattttgg 360
gca 363
```

&lt;210&gt; 346

&lt;211&gt; 2260

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2260)

<223> matrix metalloproteinase 11 (stromelysin 3)  
(MMP11) gene.

&lt;400&gt; 346

```
aagcccagca gcccggggc ggatggctcc ggccgcctgg ctccgcagcg cggccgcgcg 60
cgccctcctg ccccgatgc tgctgctgct gctccagccg ccgcccgtgc tggcccgggc 120
tctgccgccc gacgtccacc acctccatgc cgagaggagg gggccacagc cctggcatgc 180
agccctgccc agtagcccgg cacctgcccc tgccacgcag gaagcccccc ggctgcccag 240
cagcctcagg cctccccgct gtggcgtgcc cgacccatct gatgggctga gtgcccgcaa 300
ccgacagaag aggttcgtgc tttctggcgg gcgctgggag aagacggacc tcacctacag 360
gatccttcgg ttcccattgc agttggtgca ggagcaggtg cggcagacga tggcaga ggc 420
cctaaaggta tggagcgatg tgacgccact cacctttact gaggtgcacg agggccgtgc 480
tgacatcatg atcgacttgc ccaggtactg gcatggggac gacctgccgt ttgatgggcc 540
tgggggcatc ctggcccatt cttcttccc caagactcac cgagaagggg atgtccactt 600
cgactatgat gagacctgga ctatcgggga tgacc agggc acagacctgc tgcagggtggc 660
agcccataaa tttggccacg tgctggggct gcagcacaca acagcagcca aggccctgat 720
gtccgccttc tacaccttc gctacccact agtctcagc ccagatgact gcaggggcgt 780
tcaacaccta tatggccagc cctggcccac tgtcacctcc aggaccccag cctggggccc 840
ccaggctggg atagacacca atgagattgc accgctggag ccagacgccc cgccagatgc 900
ctgtgaggcc tcctttgacg cggctctccac catccgaggc gagctctttt tcttcaaagc 960
gggctttgtg tggcgccctc gtgggggcca gctgcagccc ggctaccag cattggcctc 1020
tcgccactgg cagggactgc ccagccctgt ggacgtgcc ttcgaggatg ccca gggcca 1080
catttggttc ttccaagggt ctcagtactg ggtgtacgac ggtgaaaagc cagtccctggg 1140
```

223/292

```

ccccgcaccc ctcaccgagc tgggcctggt gaggttcccc gtccatgctg ccttggtctg 1200
gggtcccgag aagaacaaga tctacttctt ccgaggcagg gactactggc gtttccaccc 1260
cagcaccggg cgtgtagaca gtcccgtgc c ccgcagggcc actgactgga gaggggtgcc 1320
ctctgagatc gacgctgcct tccaggatgc tgatggctat gcctacttcc tgcgcggccg 1380
cctctactgg aagtttgacc ctgtgaagg tgaaggctctg gaaggcttcc ccggtctcgt 1440
gggtcctgac ttctttgggt gtgccgagcc tgccaacact ttcctctgac catggcttgg 1500
atgccctcag ggggtgctgac ccctgccagg ccaogaatat caggctagag acccatggcc 1560
atctttgtgg ctgtgggcac caggcatggg actgagccca tgtctcctgc agggggatgg 1620
ggtggggtag aaccaccatg acaactgccg ggagggccac gcaggctcgt gtcacctgcc 1680
agcgactgtc tcagactggg cagggaggct ttggcatgac tt aagaggaa gggcagtctt 1740
gggaccgct atgcaggctc tggcaaacct ggctgccctg tctcatccct gtccctcagg 1800
gtagcaccat ggcaggactg ggggaactgg agtgtccttg ctgtatccct gttgtgaggt 1860
tccttcagg ggctggcact gaagcaagg tgctggggcc ccatggcctt cagccctggc 1920
tgagcaactg ggctgta ggg cagggccact tcctgaggtc aggtcttgggt aggtgcctgc 1980
atctgtctgc cttctggctg acaatcctgg aaatctgttc tccagaatcc aggccaaaaa 2040
gttcacagtc aaatggggag ggtattctt catgcaggag accccaggcc ctggaggctg 2100
caacatacct caatcctgtc ccaggccgga tcctcctgaa gcccttttcg cagcac tgct 2160
atcctccaaa gccattgtaa atgtgtgtac agtgtgtata aacottcttc ttcttttttt 2220
tttttaaaact gaggattgtc attaaacaca gttgttttct 2260

```

&lt;210&gt; 347

&lt;211&gt; 273

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(273)

<223> 3' terminal sequence. hypothetical protein  
mgc13071 (MGC13071) gene.

&lt;400&gt; 347

```

atgtttattg aacgtaacag tataattcat gtatgttccc ataatttttt catgtactaa 60
ctcatgtaat tctttgtttt ttagagatct gaagtgat tt tacctttact tccttcaatt 120
taagccaatc atgaaatttc agtgatttct ggggtgaggg cgaaagggtg tgttacgaat 180
catcgggggt gtggccagnt tgctcacgg aggtgcagg tggctggggc ctcactaggg 240
canctggagg agcacggact gcctgccgg cag 273

```

&lt;210&gt; 348

&lt;211&gt; 330

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(330)

<223> 5' terminal sequence. hypothetical protein  
mgc13071 (MGC13071) gene.

&lt;400&gt; 348

```

ggagtacaga acattgtggt aggggaagg actcactttc tcatcccatg tgtacaaaaa 60
ccaattatct ttgactgctg ttctcaacca cgtagtcgnc cagtcacac tggtagcaaa 120
gatttacaga atgtcaacat cacactgtgc atcctcttcc ggcccatcac tagccagctt 180

```



224/292

```
cctcgcatct tcaccagcat tggagaggac tacgatgagt gtgtgctgcc gttcattacc 240
acggagatcc tcaagtcact ggtggctcgc tttgatgctg gagaactaat caccagagg 300
gagcttggtt tccagccngg tgaagnacca                               330
```

&lt;210&gt; 349

&lt;211&gt; 1168

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:prime r

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1168)

<223> hypothetical protein mgc13071 (MGC13071)  
gene.

&lt;400&gt; 349

```
aaatgatgat agtagtacct acagtatagt gctgttagaa ttacatgagt tagatgtgga 60
ggtcagagtg gaagcagggtg tgagagggtc ccgcagaaga aaacatggct gccaaagtgt 120
ttgagtecat cggcaagttt ggcctggcct tagctgttgc aggaggcatg gtgacctctg 180
ccttatgtaa tgtggatgct gggcacagag ctgccatctt tgaccaattc cgtggagtac 240
agaacattgt ggtaggggaa gggactcact ttctcatccc atgtgtacaa aaaccaatta 300
tctttgactg ctgtttctcaa ccacgtagtg cgccagtcac c actggtagc aaagatttac 360
agaatgtcaa catcacactg tgcacacctt tccggcccat cactagccag ctctctcgca 420
tcttcaccag cattggagag gactacgatg agtgtgtgct gccgttcatt accacggaga 480
tcttcaagtc actggtggct cgctttgatg ctggagaact aatcacccag agggagctgg 540
tctccagcca ggtgagcaac aaccttatgg agtgagcagc cacctttggg ctctattctg 600
acgacgtgtc tttgacacat ctgaccttct tgaaggagt aacagacagg tggcccccca 660
ggaagcagag agcgccagat ttgtggtgga aaaggcggcc atcatctctg ctgaggggtg 720
ctccaaggca gctgagctga tcgccaaetc actggccact gcaggggacg gccagagcga 7 80
gctgtgcaag ctggaagctg cagaagacat tgcataccag ctctcatgct ctcggaacat 840
cacctgcctg ccggcagggc agtccgtgct cctccagctg ccctagttag gccccagcct 900
acctgcacct ccgtgaggca actgggccac agccccgatg attcgttaaca ccacctttcg 960
ccctcacccc agaaatcact gaaatttcat gattggctta aagtgaagga agtaaaggta 1020
aaatcacttc agatctctaa aaaacaaaga attacatgag ttagtacatg aaaaaattat 1080
gggaaactac atgaaatata ctgttacggt caataaacat tagcttctgt atataaaaaa 1140
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa                               1168
```

&lt;210&gt; 350

&lt;211&gt; 315

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(315)

<223> 5' terminal sequence. interleukin enhancer  
binding factor 2, 45kd (ILF2) gene.

&lt;400&gt; 350

```
ctggctttga aatcagttct ncgtgatgct acagtgaaga ttctcattac aacagtgcc 60
cccaatcttc gaaaactgga tccagaactc catttgata tcaaagtatt gcagagtgcc 120
ttagcagcca tccgacatgc ccgctggttc gaggaataatg cttctcagtc cacagttaaa 180
gttcnccanc agantactga aggacttgag gattcgtttt ccnggctttg agc cctcaca 240
```

225/292

ccnnggatnc ttgaactact aggnccattat gctgtgatga acaacccccac caganagcct 300  
ttggcnctaa acgtt 315

<210> 351  
<211> 1552  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1552)  
<223> interleukin enhancer binding factor 2, 45kd  
(ILF2) gene.

<400> 351  
cggttggtgc ggccctccatt gttcgtgttt taaggcgcca tgaggggtga cagaggccgt 60  
ggtcgtgggtg ggcgcttttg ttccagagga ggcccaggag gag gggtcag gccctttgta 120  
ccacatatcc catttgactt ctatttgtgt gaaatggcct tccccgggt caagccagca 180  
cctgatgaaa ctctcttcag tgaggccttg ctgaagagga atcaggacct ggctcccaat 240  
tctgctgaac aggcattctat ctttctcttg gtgacaaaaa taaacaatgt gattgataat 300  
ctgattgtgg ctccagggac a ttgaagtg caaattgaag aagttcgaca ggtgggatcc 360  
tataaaaagg ggacaatgac tacaggacac aatgtggctg acctgggtgg gatactcaag 420  
attctgccaa cgttggaagc tgttgctgcc ctggggaaca aagtcgtgga aagcctaaga 480  
gcacaggatc cttctgaagt ttttaaccatg ctgaccaacg aaactggctt tgaaatcagt 540  
tcttctgatg ctacagtga gattctcatt acaacagtgc cacccaatct tcgaaaactg 600  
gatccagaac tccatttgga tatcaaagta ttgcagagtg ccttagcagc catccgacat 660  
gcccgctggt tcgaggaaaa tgcttctcag tccacagtta aagttctcat cagactactg 720  
aaggacttga ggattcgctt tcttggtctt gagccccca c acctggat ccttgacct 780  
ctaggccatt atgctgtgat gaacaacccc accagacagc ctttgccct aaacgttgca 840  
tacaggcgct gcttgcatg tctggctgca ggactgttc tgccagggtc agtgggtatc 900  
actgaccct gtgagagtgg caactttaga gtacacacag tcatgacct agaacagcag 960  
gacatggtct gctatacagc tcagactctc gtccgaatcc tctcatggtg tggctttagg 1020  
aagatccttg gccaggagg tgatgccagc tatcttgctt ctgaaatct tacctgggat 1080  
ggagtgatag taacaccttc agaaaaggct tatgagaagc caccagagaa gaaggaagga 1140  
gaggaagaag aggagaatac agaaagaacc acctcaagga gaggaagaag aaagcatgg a 1200  
aactcaggag tgacattccc ttcactcctt ttcctaccca agggaaagac tggagcctaa 1260  
gctgcctgct actggcttta catggtgaca gacattccgt ggataggaag atagcaggag 1320  
aaagtaactc catagagtgt cattccactg gttgatattg gcttagctgc cagtctccca 1380  
tttgtgacct atgccatcca tctataatgg agg ataccaa catttcttcc taatattcta 1440  
taatctccaa ctctgaaaa cccctctctc aactaatact ttgctgttga aatgttgtga 1500  
aatgttaagt gtctggaaat ttttttttct aagaaaaact attaaagtac tt 1552

<210> 352  
<211> 396  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(396)  
<223> 3' terminal sequence. hypothetical protein  
flj11307 (FLJ11307) gene.

226/292

&lt;400&gt; 352

```
ctccattaca ggggtttttgc cacttgctgt gaggataggg ccctgagttc ttacctctaa 60
ggtactggag gtttc agttg tagaatttcc agtattattg cttgagtttg aagacactgt 120
ttcattttta ctttcattat ctgatttttc atcggaactc atacattcaa tatctgcatc 180
aaagcctgtt ggatatccca ttgcctgcaa taccttcacc gctacgtgaa agttttgctg 240
ttttcttgga tggctcctgag gcttcataatg ttgtgccatc cacatctaca gacattg tga 300
agactggggg catgaacggg ggccagactg aagataagaa gctatactga agcacaggcc 360
tgatctgaat taagcntcat tagtggcatt ccataa 396
```

&lt;210&gt; 353

&lt;211&gt; 1858

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1858)

<223> hypothetical protein flj11307 (FLJ11307)  
gene.

&lt;400&gt; 353

```
tcgatgaaag atcctccgga cttattggac aggcagaaat gcccgaacgc cttggcgtct 60
cttcgacatg ccaaattggtt tcaggcaagg gcaaattgat taaaatcatg tgtaat tgtc 120
ctccgattc tgctgattt gtgcaacaga gtcccacat gggcaccatt gaaaggatgg 180
ccactagaac ttatatgtga aaagtctata ggtacttgta atagaccttt gggcgctggg 240
gaggccttga gacgagtaat ggagtgtttg gcatctggaa tactacttcc tgggggtcct 300
ggtcttcatg atccttgtga gcgagacca acag atgctc tgagctatat gaccatccag 360
caaaaaagaag atattaccca cagtgcacag catgcaactc gactatcagc ctttgccag 420
atttacaagg tgctggagat ggacccctt ccatctagta agccttttca gaagtattcc 480
tggtcagtta ctgataaaga aggtgctggg tcttcagctc taaagaggcc atttgaagat 540
ggattagggg atgataaaga cccaacaag aagatgaaac gaaacttaag gaaaattctg 600
gatagtaaag caatagacct tatgaatgca ctaatgaggc taaatcagat caggcctggg 660
cttcagtata agctcctatc tcagtctggc cccgttcatg cccagctctt cacaatgtct 720
gtagatgtgg atggcacaac atatgaagcc tcaggacat ccaagaaaac agca aaactt 780
cacgtagcgg tgaagggtatt gcaggcaatg ggatatccaa caggccttga tgcagatatt 840
gaatgtatga gttccgatga aaaatcagat aatgaaagta aaaatgaaac agtgtcttca 900
aactcaagca ataatactgg aaattctaca actgaaacct ccagtacctt agaggtaaga 960
actcagggcc ctatcctcac agcaagtggc aa aaacctg taatggagct caatgaaaaa 1020
agaagaggtc tcaagtatga actcatctca gagactggtg gaagccatga caagcgttt 1080
gtaatggagg tagaagtaga tggacagaaa ttcagaggcg cagggtccaa taagaaagt 1140
gcaaaggcga gtgcagcttt agctgccttg gagaaactgt tttctggacc caatgcggca 1200
aataataaga aaaagaagat tatccctcag gcaaaggcg ttgtgaatac agctgtgtct 1260
gcagcagtc aagctgttcg gggcagagga agaggaaactc taacaagggg agcttttgtt 1320
ggggcgacag ctgctcctg ctacatagct ccaggctatg gaacaccata tggttacagc 1380
acagctgccc ctgcctatgg ttaccceaag agaattggtc tggtac ccgt tatgaaattt 1440
ccaacatata ctgttcccca ctactcattc ttttagcaaa tgacagaagc taattcctat 1500
tgaacaacaa tacagtacaa cacagaatgt tagagaaaaa gcctttttat cctgtcttct 1560
ttgaacacat acttgatcaa aattatttgt aaagaacatc tttcctactt tttgatttta 1620
acaaatgcaa atttagttct ctaaaacttg aaaaaaaaaa aagaaaccag ttctgtgaaa 1680
acggtacctc atttctggaa aataacttat accagccctt ctgttctagg gaaataaaag 1740
tctagcagtt caaagttaa gttttaagag acgtatcaga ttatgtaaaa ttaattttgt 1800
gaaggatgta tagagtctca aacactgatc acaataaac tgctttgtg taacacag 1858
```

&lt;210&gt; 354

&lt;211&gt; 242

&lt;212&gt; DNA

227/292

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(242)

&lt;223&gt; 5' terminal sequence. v-myb avian

myeloblastosis viral oncogene homolog (MYB) gen e.

&lt;400&gt; 354

```
agaaccccag ctatcaaaag gtcaatctta gaaagctctc caagaactcc tacaccattc 60
aaacatgcac ttgcagctca agaaattaaa tacgggtcccc tgaagatgct acctcagaca 120
ccctctcatc tagtagaaga tctgcaggat gtgatcaaac aggaatctga tgaatctgga 180
attgttgctg agtttcaacg aaaatggacc acccttactg aacgaaaatc ntacaacgag 240
gt                                         242
```

&lt;210&gt; 355

&lt;211&gt; 3225

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3225)

<223> v-myb avian myeloblastosis viral oncogene  
homolog (MYB) gene.

&lt;400&gt; 355

```
ggcggcagcg ccctgccgac gccggggagg gacgcaggca ggcggcgggc agcgggaggc 60
ggcaccgccg tgctccccgc ggctctcggc ggagccccgc cgcccgccgc gccatggccc 120
gaaagaccgc gcacagcata tatagcagtg acgaggatga tgaggacttt gagatgtgtg 180
accatgacta tgatgggctg cttcccaagt ctggaaagcg tcacttgggg aaaacaagggt 240
ggaccgggga agaggatgaa aaactgaaga agctgggtgga acagaatgga acagatgact 300
ggaaagtatt tgccaattat ctccgaatc gaacagatgt gcagtgccag caccgat ggc 360
agaaagtact aaacctgag ctcatacagg gtccctggac caaagaagaa gatcagagag 420
tgatagagct tgtacagaaa tacgggtccga aacgttggtc tgttattgcc aagcacttaa 480
agggggagaat tggaaaacaa tgtagggaga ggtggcataa ccacttgaat ccagaagtta 540
agaaaacctc ctggacagaa gaggaagaca gaatt attta ccaggcacac aagagactgg 600
ggaacagatg ggcagaaaatc gcaaagctac tgcctggacg aactgataat gctatcaaga 660
accactggaa ttctacaatg cgtcggaagg tgcgaacagga aggttatctg caggagtctt 720
caaaagccag ccagccagca gtggccacaa gcttcagaa gaacagtcac ttgatgggtt 780
ttgctcaggc tccgcctaca gctcaactcc ctgccactgg ccagcccact gttaacaacg 840
actattccta ttaccacatt tctgaagcac aaaatgtctc cagtcattgt ccataccctg 900
tagcggttaca tgtaaatata gtcaatgtcc ctccagcagc tgccgcagcc attcagagac 960
actataatga tgaagaccct gagaaggaaa agcgaataaa ggaattagaa ttgct cctaa 1020
tgtcaaccga gaatgagcta aaaggacagc aggtgtctacc aacacagaac cacacatgca 1080
gctaccccggt gtggcacagc accaccattg ccgaccacac cagacctcat ggagacagtg 1140
cacctgtttc ctgtttggga gaacaccact ccactccatc tctgccagcg gatcctggct 1200
ccctacctga agaaagcgcc tcgccagcaa ggtgcatgat cgtccaccag ggcaccattc 1260
tgataatgt taagaacctc ttagaatttg cagaaacact ccaatttata gattctttct 1320
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ccctcattgg tcacaaattg actgttacaa caccatttca tagagaccag actgtgaaaa 1440
ctcaaaagga aaatactgtt tttagaacct cagctatcaa aaggtcaatc ttagaaagct 1500
ctccaagaac tcctacacca ttcaaactg cacttgacgc tcaagaaatt aaatacggtc 1560
ccctgaagat gctacctcag acaccctctc atctagtaga agatctgcag gatgtgatca 1620
```

228/292

```

aacaggaatc tgatgaatct ggatttgttg ctgagtttca aga aaatgga ccacccttac 1680
tgaagaaaat caaacaagag gtggaatctc caactgataa atcaggaaac ttcttctgct 1740
cacaccactg ggaaggggac agtctgaata cccaactgtt cacgcagacc tcgcctgtgc 1800
gagatgcacc gaatatctct acaagctccg ttttaatggc accagcatca gaagatgaag 1860
acaatgttct caaagcat tt acagtaccta aaaacaggtc cctggcgagc cccttgacgc 1920
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gattttttaa aataaataac agtcttacct aaattattag gtaatgaatt gtagccagtt 2280
gttaatatct taatgcagat ttttttaaaa aaaaacataa aatgatattat ctggtatttt 2340
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tcagtaaaaa cattactcta agttagact taataccatg tgacatttaa tccagattgt 2520
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attttttatt tgggtttttt tgttattggt ggtttataca agcatgcgtt gcacttcttt 2940
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gtcactgcct taagaacatt tgatgcaaga tggccagcac tgaacttttg agatatgac g 3180
gtgtacttac tgccttgtag caaaataaag atgtgccctt atttt 3225

```

&lt;210&gt; 356

&lt;211&gt; 369

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(369)

<223> 3' terminal sequence. zinc finger protein 9  
(a cellular retroviral nucleic acid binding  
protein) (ZNF9) gene.

&lt;400&gt; 356

```

gtagttaa at gcagaaagtc ggtttttttc caccctttc ctctttttac acggcaagta 60
aagctcactg gcttgggagt tgcctctatc tgccaacctt tggccagtga agaggattca 1 20
gagaaaaata tacaaccatc aatcagaaaa agggagggcg acaaaggaaa ataattaggc 180
tgtagctcaa ttgtgcatc cgtgcaagg tggcctgact cgccacagcg gtaacagttg 240
acttcacttg tcttgcctga gttgatggct acatgaccag tttcaccaca cctatagcac 300
ttcacttttg tgcagtcttt ttggaatgtg tcccgaattc tcccacaaga atancctttc 360
tgtctcanc 369

```

&lt;210&gt; 357

&lt;211&gt; 1500

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1500)  
<223> zinc finger protein 9 (a cellular retroviral  
nucleic acid binding protein) (ZNF9) gene.

<400> 357  
gaattccaaa cagcctctac cttgcgagcc gtcttcccca ggctgcgctc cgagtctccg 60  
ccgctgcggg cccgctccga cgcggaagat ctgactgcag ccatgagcag caatgagtgc 120  
ttcaagtgtg gacgatctgg ccactgggccc cgggaatgtc ctactggtgg aggccgtggg 180  
cgtggaatga gaagccgtgg cagagggtgtt ttacctcgg atagagggtt ccagtttgtt 240  
tctcgtctc ttccagatat ttgttatcgc tgtggtgagt ctgggtcatct tgccaaggat 300  
tgtgatcttc aggaggatgc ctgctataac tgcggtagag gtg gccacat tgccaaggac 360  
tgcaaggagc ccaagagaga gcgagagcaa tgcgtctaca actgtggcaa accaggccat 420  
ctggctcgtg actgcgacca tgcatgag cagaaatgct attcttggg agaattcgga 480  
cacattcaaa aagactgcac caaagtgaag tgctataggt gtggtgaaac tggcatgta 540  
gccatcaact gcagcaagac a agtgaagtc aactgttacc gctgtggcga gtcagggcac 600  
cttgacggg aatgcacaat tgaggctaca gcctaattat ttcccttctg cgccctcct 660  
ttttctgatt gatggttcta ttattttctc tgaatcctct tcaactggca aggttggca 720  
gatagaggca actcccaggc cagtgaagct tacttgccgt gtaaaaggag gaaaggggtg 780  
gaaaaaacc gactttctgc atttaactac aaaaaaagt tatgtttagt ttggtagagg 840  
tgttatgtat aatgctttgt taaagaacct cctttccgt ccactggtga atagggattg 900  
atgaatggga agagttgagt cagaccagta agcccgctc gggttccttg aacatgttcc 960  
catgtaggag gtaaaaccaa ttctggaagt gtctatgaac t tccataaat aactttaatt 1020  
ttagtataat gatggtcttg gattgtctga cctcagtagc tattaataa catcaagtaa 1080  
catctgtatc aggcctaca tagaacatac agttgagtg gagtaacaa aaagataaac 1140  
atgcgtgtta atggctgttc gagagaaatc ggaataaaag cctaaacagg aacaacttca 1200  
tcacagtgtt gatgtt ggac acatagatgg tgatggcaaa ggtttagaac acattatatt 1260  
caaagactaa atctaaaacc cagagtaaac atcaatgctc agagtttagc taatttggag 1320  
ctattcagga attgcagaga aatgcatttt cacagaaatc aagatgttat tttgtatac 1380  
tatacactt agacaactgt gtttcatttg ctgtaatcag tttttaaag tcaga tggaa 1440  
agagcaactg aagtctaga aaatagaaat gtaattttaa actattccaa taaagctgga 1500

<210> 358  
<211> 425  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(425)  
<223> 3' terminal sequence. camp responsive  
element modulator (CREM) gene.

<400> 358  
ttttttactt ctgcaagatc ttttatatta cacagtagag ttaaaaactg tagtaaatgt 60  
tcagatatth aaatgagcac caaacactac aaagtgaac caacatggtt ctattaaaaa 120  
ctcncctttg ctatggcatt caaggacagc aatacaat ct tttttttttt taacaaagca 180  
actaatataa aaatctgcaa atgccatata ttcatatcta ggctattctt cncatatagg 240  
catgtcatta gatagacttt ctttctatcc ttccngagg natttttttg nggtttacnt 300  
ttattgnact gctggatgca ttatttttga tcatcctttc ctaaaatgnt ttaaagacct 360  
gcaataaatt ttattg cata ggacacnatt ggtgncacat agaatgggag cngcaagtat 420  
gtggc 425

<210> 359

230/292

<211> 232  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(232)  
<223> 5' terminal sequence. camp responsive  
element modulator (CREM) gene.

<400> 359  
ggatttagag ttaactagct caccactgcc tctgcctcca agctgccttt tagactgaat 60  
agcttttctt gttagcccta ctttaacatt tcttttgaag tgggtgtctg cttgaagagg 120  
gaaacacgtc atgaaactgt aatgcatgaa cagaactcag gagttgtctg gccagcttag 180  
tgctgccact ggtgacatgc caacttacca gatccgagct cctantgnng ct 232

<210> 360  
<211> 1431  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:prime r

<220>  
<221> misc\_feature  
<222> (1)..(1431)  
<223> camp responsive element modulator (CREM)  
gene.

<400> 360  
atgaccatgg aaacagttga atcccagcat gatggaagta taacagcttc tttgacagag 60  
agcaagtctg ctcatgtgca gactcagact gggcaaattt caatccctgc tttagctcag 120  
tgcaagtgagc tgagatcagg caccagaaga ggctcccag ctgtaactct agtgcaagta 180  
ccttcggggc aaactataca tgtccaggga gtaattcaga caccacagcc atgggttatt 240  
cagtcacatc aaatacacac cgttcaggta gcagcaattg cagagacaga tgaatctgca 300  
gaatcagaag gtgtaattga ttctcataaa cgtagagaaa t cctttcacg aagaccctct 360  
tataggaaaa tactgaatga actgtcctct gatgtgcctg gtgttcccaa gattgaagaa 420  
gagagatcag aggaagaagg aacaccacct agtattgcta ccatggcagt accaactagc 480  
atatacaga ctagcacggg gcaatacatt gctatagccc aagggtggaac aatccagatt 540  
tctaaccagc gatctgatgg tgttcaggga ctgcaggcat taacaatgac aaattcagga 600  
gctcctccac caggtgctac aattgtacag tacgcagcac aatcagctga tggcacacag 660  
cagttctttg tcccaggcag ccaggttgtt gttcaagctg ccactggtga catgccaaact 720  
taccagatcc gagctcctac tgctgctttg ccacaggag tggtgatggc tgcacgccc 780  
ggaagtgtgc acagtcccca gcagctggca gaagaagcaa cagcgaacg agagctgagg 840  
ctaataaaaa acagagaagc tgcccgggag tgtcgcagga agaagaaaga atatgtcaaa 900  
tgtcttgaaa atcgtgtggc tgtgcttgaa aaccaaaca agactctcat tgaggaaactc 960  
aaggccctca aagatcttta ttgccataaa gtagagtaac tgtctttgac ttggaccttg 1020  
tttactctaa tcaaggcagg agatgcagca gtcctactta ttgccatgtg gacttgtggg 1080  
aaggacacgt gtgaccctta agaatccagt ttggattagt gtttgaaatt gaattgggaa 1140  
tgttgttcca ggaatgtgaa tgcagcgtga tcacacttac cgagcttact ttgatctgtt 1200  
tgtcaatagc atgcataaaa tgctttgttt gccctttgct tctgcttttt ttcagggaag 1260  
ctgccaaaaga atgtcgacgt cgaaagaaag aatatgtaaa atgcctggag agccgagttg 1320  
cagtgctgga agtccagaac aagaagctta tagaggaact tgaaacctg aaagacattt 1380  
gttctcccaa aactgattac tagaaatatt taactatgaa ctgattacag a 1431

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<210> 361  
<211> 457  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(457)  
<223> 3' terminal sequence. cathepsin b (CTSB)  
gene.

<400> 361  
caagttggag aaacctttaa ttggcacagg cattccttgt taacttgaca gggatgaagct 60  
gtaatttttc aaaaacagta aaagctggtt tctcctaaac tattttcctt gtggtagtag 120  
agatcagtgg gtcagaaaca actcctgacc acttggtttc cttttgagcc gcgtcattag 180  
gaggcaatct gtaaaactag cacaggtctc ccgctgttcc actggctcac ccacatg att 240  
agcagagtgc acgaaaaaat aaaacttcta ttaaagaatc atgctgagca caacatcaga 300  
gaggtttgtga cattgcaaac tcgatagatg cagggggcct gggagactgg cgttctccaa 360  
agggctccca acaccatctc tcctctgatt tctgtgacaa atgtggaagc tacttgcttg 420  
gaggtactgg gggaactgat gggggaactt tcac cg 457

<210> 362  
<211> 401  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(401)  
<223> 3' terminal sequence. melan -a (MLANA) gene.

<400> 362  
atcatgcatt gcaacattta ttgatggagt tttcccaatt taatatttct catcatttcc 60  
tcacatgatt agtactgcta gcggacctac taaaatttta acactgactt attattagag 120  
atggcttgca tttttcctac accattccaa aggagaacat tagatgtctg tattaattc 180  
aagcaaaagt gtgagagaaa taatttcagc atgtctcagg tgtctcgt g gnccttaagg 240  
tgaataagggt ggtggtgact gttctgcaga gagtttctca taagcagggt gagcattggg 300  
aaccacagggt tcacagtttt tctcttgaag agacactttg ctgtcccgat gatcaaacc 360  
ttcttggtgg catcttcctg ttaaggcaca ttgaggccaa c 401

<210> 363  
<211> 370  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(370)  
<223> 5' terminal sequence. melan -a (MLANA) gene.



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&lt;400&gt; 363

```
attaaggaag gtgtcctgtg ccctgaccct acaagatgcc aagagaagat gctcacttca 6 0
tctatggtta cccaagaag gggcacggcc actottacac cacggctgaa gaggccgctg 120
ggatcggcat cctgacagtg atcctgggag tcttactgct catcggctgt tggatttgta 180
gaagacgaaa tggatacaga gccttgatgg ataaaagtct tcatgttggc actcaatgtg 240
cttaacaaga agatgccac aagaagggtt tgatcatcgg gacagcaaag tgtctcttca 300
agagaaaaac tgtgaacctg tggttcccaa tgcctccact gcttatggag aaactctctg 360
cagaacagtc                                     370
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&lt;210&gt; 364

&lt;211&gt; 1524

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1524)

&lt;223&gt; melan-a (MLANA) gene.

&lt;400&gt; 364

```
agcagacaga ggactctcat taaggaaggt gtcctgtgcc ctgaccctac aagatgcca 60
gagaagatgc tcaattcatc tatggttacc ccaagaaggg gcacggccac tcttacacca 120
cggctgaaga ggccgctggg atcggcatcc tgacagtgat cctgggagtc ttactgctca 180
tcggctgttg gtattgtaga agacgaaatg gatacagagc cttgatggat aaaagtcttc 240
atgttggcac tcaatgtgcc ttaacaagaa gatgccaca agaagggtt gatcatcggg 300
acagcaaatg gtctcttcaa gagaaaaact gtgaacctgt ggttccc aat gctccacctg 360
cttatgagaa actctctgca gaacagtcac caccacctta ttcacctta gagccagcga 420
gacacctgag acatgctgaa attatttctc tcacactttt gcttgaattt aatacagaca 480
tctaattgtt tcctttggaa tgggttagga aaaatgcaag ccatctctaa taataagtca 540
gtgttaaaat ttagtaggt cgcct agcag tactaatcat gtgaggaaat gatgagaaat 600
attaatttg gaaaactcca tcaataaatg ttgcaatgca tgatactatc tgtgccagag 660
gtaattgttag taaatccatg gtgttatttt ctgagagaca gaattcaagt gggatttctg 720
gggccatcca atttctcttt acttgaaatt tggctaataa caaactagtc aggttttcga 780
accttgaccg acatgaactg tacacagaat tgttccagta ctatggagtg ctcacaaagg 840
atacttttac aggttaagac aaagggttga ctggcctatt tatctgatca agaacatgtc 900
agcaatgtct ctttgtgctc taaaattcta ttatactaca ataatatatt gtaaatatcc 960
tatagctctt tttttttgag atggagtttc gcttttgttg cccag gctgg agtgcaatgg 1020
cgcgatcttg gctcaccata acctccgct cccaggttca agcaattctc ctgccttagc 1080
ctcctgagta gctgggatta caggcgtgcg ccactatgcc tgactaatth ttagtthtta 1140
gtagagacgg ggtttctcca tgttggtcag gctgggtctc aactcctgac ctcaggtgat 1200
ctgcccgcct cagcctccca aagtgtctga attacaggc tgagccacca cgctggctg 1260
gatcctatat cttaggtaag acatataacg cagtctaatt acatttctact tcaaggctca 1320
atgctattct aactaatgac aagtattttc tactaaacca gaaattggta gaaggattta 1380
aataagtaaa agctactatg tactgcctta gtgctgatgc ctgtgtactg ccttaaatg t 1440
acctatggca atttagctct cttgggttcc caaatccctc tcacaagaat gtgcagaaga 1500
aatcataaag gatcagagat tctg                                     1524
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&lt;210&gt; 365

&lt;211&gt; 556

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:p rimer

&lt;220&gt;

233/292

<221> misc\_feature  
<222> (1)..(556)  
<223> 3' terminal sequence. apr -1 protein (APR-1)  
gene.

<400> 365  
actattcggt aggtttttat ttttctctat gttctgcagt aactaaggaa aatcatggta 60  
aatgtcaatc ttcacacaac agcagacaca aagggtttca gaaacgtcag atatgaag aa 120  
atctccatc cttcttcaac attttactgg gtatttcaac ttcaaaagaa cagcttattt 180  
ctataagtgc tgtacaagat catagattat gatggaacga cttcatttta gaacgttagc 240  
aaaactgtta tactaaatgt caatgacagg aaacaaagaa aaaaatttgt tcaattatat 300  
ttttaaacat attgttattc tcaacaaacg gaattt taaa acgaatacaa ttttccatta 360  
tcaaaaagca aacactctat ttgcagttg aacaatgac actgacaca aatatacnaat 420  
acagtgtccc ccgcccccaa tcgacatcat tttccactta gggaccctgg catccactcc 480  
ctgggggtac ccgtgactcc ncctttacac cccccagggg ctggcctcag atctacctaa 540  
gggnggggat aacc cc 556

<210> 366  
<211> 464  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(464)  
<223> 5' terminal sequence. apr -1 protein (APR-1)  
gene.

<400> 366  
aacagcgcca aggaagctct ggtctggaaa gtgctgggga agttaggaat gcagcctgga 60  
cgtcagcaca gcatcttttg agatccgaag aagatcgtca cagaagagtt tgtgcgcaga 120  
gggtacctga ttataaaacc ggtgccccgt agcagtcagg tggagtatga gttcttctgg 180  
gggccccgag cacacg tgga atcgagcaaa ctgaaagtca tgcattttgt ggcaagggtt 240  
cgtaaccgat gctctaaaga ctggccttgt aattatgact gggattcggga cgatgatgca 300  
gagggttgagg ctatcctcaa ttcagggtgct aggggttatt ccgcccccta agtagatctg 360  
gaggcagacc cttgggggtt gtaaaagaga gtnacaggta cccccaaagg agtagatg nc 420  
aaggggccct aagttgcaaa atgatgtcga ttttggggcc gggg 464

<210> 367  
<211> 1476  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1476)  
<223> apr-1 protein (APR-1) gene.

<400> 367  
ctggaagaat tcgcgtggca ggagaggcgg ggccaatttt gctgagcttt ctgcggggct 60  
tgcagctgcg gcaagtgcgt gcggcggctg ctgcgcgaag tcagctggcg tgggaactac 120  
cctttgtagc tgagaacggc ttgtttattg ctacaaagac totattgaca ttggtagctt 180  
cagcggcagc agcttct tac ggtataaagc tggtgcttcc tgaagaggct acaagcatcc 240

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ttccctagga ctgctgtaag ctttgagcct ctagcaggag acatgcctcg gggacgaaag 300
agtgcggccc gccgtaatgc gagagccgca gaagagaacc gcaacaatcg caaaatccag 360
gcctcagagg cctccgagac ccctatggcc gcctctgtgg tagcgagcac ccccgaaga c 420
gacctgagcg gccccgagga agacccgagc actccagagg aggctctac caccctgaa 480
gaagcctcga gcaactgcca agcacaaaag ctttcagtgc cccggagcaa ttttcagggc 540
accaagaaaa gtctcctgat gtctatatta gcgctcatct tcatcatggg caacagcgcc 600
aaggaagctc tggcttgga agtgctgggg aagttag gaa tgcagcctgg acgtcagcac 660
agcatctttg gagatccgaa gaagatcgtc acagaagagt ttgtgocgag agggtagctg 720
atttataaac cgggtgcccc tagcagtcgc gtggagtatg agttcttctg ggggccccga 780
gcacacgtgg aatcgagcaa actgaaagtc atgcattttg tggcaagggt tcgtaaccga 840
tgctctaaag actggccttg taattatgac tgggattcgg acgatgatgc agaggttgag 900
gctatcctca attcagggtc taggggttat tccgcccctt aagtagatct gaggcagacc 960
cttgggggtg taaaagagag tcacaggtag cccaaggagt agatgccagg gtcctaagtt 1020
gaaaatgatg tcgattgggg gcgggggaca ctgtatttga tatttgtgat cagtga tcat 1080
tgttcaactg cgaaatagag tgtttgcttt tgataatgga aaattgtatt cgttttaaaa 1140
ttcgtttgtg tgagaataac aatatgttta aaaatataat tgaacaaatt tttttctttg 1200
tttctgtca ttgacattta gtataacagt tttgctaacg ttctaaaatg aagtcgttcc 1260
atcataatct atgatcttgt acagcactta tagaaataag ctgttctttt gaagttgaaa 1320
taccagtaaa aatgttgaaag aaggatggag gatttcttca tatctgacgt ttctgaaacc 1380
ctttgtgtct gctgttgtgt gaagattgac atttaccatg attttcctta gttacttgac 1440
gtcttgtatc tctttttatt ttcggattgc ttatca 1476
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&lt;210&gt; 368

&lt;211&gt; 436

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(436)

<223> 3' terminal sequence. ets variant gene 5  
(ets-related molecule) (ETV5) gene.

&lt;400&gt; 368

```
cgtttttttg ctttaataac caaaactaca aaaatcagtt tataaactgt ttttccaaaa 60
caaccaccaa aacaaaacaa tcccccaaat cagggcaaaa caaaatactg tcaaaagtgt 120
taatcgccct tctcctaaaa taaaagtcac ccacactcag ccacgtgatt ggaagagaa 180
agggggcttg ctctacttgg cgaccacatg gccgggtggg tcccaa gagt agccatgggt 240
tatgatattg agaaccacgg agngcgaaac agctgttctg actgcccccc tttttctaga 300
caaggggtaa tatttcagat tcagctagaa gagctttcca atgtttaaga tgtattttta 360
acccttaatg gtttgagcct cccaactta gcctacttac ttttconaagg gtttgtgatt 420
tttcaacaaa ttgtgc 436
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&lt;210&gt; 369

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(414)

<223> 5' terminal sequence. ets variant gene 5  
(ets-related molecule) (ETV5) gene.

<400> 369  
ggttgctcgg cgctggggca tccagaagaa ccggccagcc atgaactatg acaagctgag 60  
ccgctctctc cgctattact atgaaaaggg catcatgcag aaggtagctg gagagcgata 120  
cgtctacaaa ttgtctctgt acccagatgc cctcttctcc atggctttcc cggataacca 180  
gcgtccgttc ctgaaggcag agtccgagtg ccacctcagc gaggaggaca cctgcccgt 240  
gaccacttt gaagacagcc ccgcttacct cctggacatg gaccgctgca gcagcctccc 300  
ctatgccgaa ggtttgctta ctaagtttct gagtggcgga gtgnccaaac cctaggagct 360  
agcagttccc attcagggca aacaagnngc agtgnggtt gtt ttgtgtt tttt 414

<210> 370

<211> 249

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(249)

<223> 5' terminal sequence. cd69 antigen (p60,  
early t-cell activation antigen) (CD69) gene.

<400> 370

ataataagga aacgtgttca cttattgact attatagaat ggaactcatg gaaatctgtg 60  
tcagtggatg ctgctctgtg gtccgaagtc ttccatagag actttgtgaa aaaaaatttt 120  
atagtgtctt gggaattttc ttccaaacag aactatggaa aaaaaggaag aaattccagg 180  
aaaatctgca ctgtgggctt ttattgccat gagctagaag catcacaggg tgaccaataa 240  
cccngacgc 249

<210> 371

<211> 1702

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(1702)

<223> cd69 antigen (p60, early t-cell activation  
antigen) (CD69) gene.

<400> 371

agactcaaca agagctccag caaagaacttt cactgtagct tgacttgacc tgagattaac 60  
tagggaatct tgagaataaa gatgagctct gaaaattgtt tcgtagcaga gaacagct ct 120  
ttgcatccgg agagtggaca agaaaatgat gccaccagtc ccattttctc aacacgtcat 180  
gaagggctct tccaagttcc tgcctgtgt gctgtaatga atgtggtctt catcaccatt 240  
ttaatcatag ctctcattgc cttatcagtg ggccaatata attgtccagg ccaatacaca 300  
ttctcaatgc catcagacag ccagtgttct tcatgc tctg aggactgggt tggtaccag 360  
aggaaatgct actttatttc tactgtgaag aggagctgga cttcagccca aaatgcttgt 420  
tctgaacatg gtgctactct tgcgtgcatt gattctgaaa aggacatgaa ctttctaaaa 480  
cgatacgag gtagagagga aactgggtt ggactgaaaa aggaacctgg tcacctatgg 540  
aagtgtgcaa atggcaaaga atttaacaac tggttcaacg ttacagggtc tgacaagtgt 600  
gtttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaattt atactggata 660  
tgtaacaaac cttacaaata ataaggaaac atgttcactt attgactatt atagaatgga 720  
actcaaggaa atctgtgtca gtgatgctg ctctgtggtc cgaagtcttc cataga gact 780

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ttgtgaaaaa aaattttata gtgtcttggg aattttcttc caaacagAAC tatggaaaaa 840
aaggaagaaa ttccaggaaa atctgcactg tgggctttta ttgccatgag ctagaagcat 900
cacaggttga ccaataacca tgcccaagaa tgagaagaat gactatgcaa cctttggatg 960
cactttatat tattttgaat ccagaaataa tgaa ataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcatgcatt tgcactactg gaaggagtta 1080
gatgttggtg ctagatactg aatgtaaaca aaggaattat ggctggtaac atagggtttt 1140
agtctaattg aatcccttaa actcaggag catttataaa tggacaaatg cttatgaaac 1200
taagatttgt aatatttctc tctttttaga gaaatttgcc aatttacttt gttatttttc 1260
cccaaaaaa atgggatgat cgtgtattta ttttttact tctcagctg tagacaggtc 1320
cttttcgatg gtacatattt ctttgccttt ataactttt atacagtgtc ttacagagaa 1380
aagacataag caaagactat gaggaatatt tgcaagacat agaatagt gt tggaaaatgt 1440
gcaatatgtg atgtggcaaa tctctattag gaaatttct gtaatcttca gacctagaat 1500
aatactagtc ttataatagg tttgtgactt tcctaaatca attctattac gtgcaatact 1560
tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt 1620
tcagtacaat tataagctgt tt ttatatat gtgaaataaa agtagaataa acacaaaaaa 1680
aaaaaaaaa aaaaaaaaaa aa                                     1702

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&lt;210&gt; 372

&lt;211&gt; 585

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(585)

&lt;223&gt; 3' terminal sequence. oncogene tc21 (TC21) gene.

&lt;400&gt; 372

```

gtaggcagta tgattccaaa agttaaaaat tatttcacaa cctgtagctt cagcttggca 60
aacagcttag attccaaaac tgattcatct ctattaaaat gtaagcactt aaaaaaagag 120
catgtctgtg tatatagaca tat atttttaa aggaatcaga taatctttga agcagcctta 180
gtgtttcctt taaatttgtc tggaaatgac cattgtatta gcttcacaga aaggactagc 240
cagcttcttc gtctaaggct aacatggtga tcatttgtct aaggctagaa aggtaccaac 300
aagatgtaaa ctgaggagag aaagagaaga tgagggcttt tcttgccgt tggtagctaa 360
aactgaaggg attctagaaa atgacacaat ggcagccttt cntgtctttt tctttccgtg 420
ttggttcngg tgaaggagga cattcctggc cctggaaatt tccnggataa cccggacaag 480
ttcatgggaa agcttgatct acattcatcc taatccttgc oggatgcnc catgtatgtt 540
acctaagctg ccggcaacgg tngcctctnc cggggtaccg gcc ng          585

```

&lt;210&gt; 373

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(451)

&lt;223&gt; 5' terminal sequence. oncogene tc21 (TC21) gene.

&lt;400&gt; 373

```

gattcttaca caaagcagtg tgtgatagat gacagagcag cccggctaga tattttggat 60

```

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```

acagcaggac aagaagagtt tggagccatg agagaacagt atatgaggac tggcgaaggc 120
ttcctgttgg tcttttcagt cacagataga ggcagttttg aagaaatcta taagtttcaa 180
agacagattc tcagagtaaa ggatcgtgat gagttcccaa tgattt taat tggtaataaa 240
gcagatctgg atcatcaaag acaggtaaca caggaagaag gacaacagtt agcacggcag 300
cttaaggtaa catacatgga ggcacagca aagattagga tgaatgtaga tcaantttcc 360
atgaacttgt ccgggttatac aggaaatttc aagancagga atgtcctctt cacagaccac 420
acggaaagaa aagccagaaa gctg cattgt g
                                         451

```

&lt;210&gt; 374

&lt;211&gt; 425

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(425)

<223> 3' terminal sequence. cd44 antigen (homing  
function and indian blood group system) (CD44)  
gene.

&lt;400&gt; 374

```

gaagatcgaa gaagtacaga tatttattat gaatcagttt aaaccctttt gtgcctctga 60
caaagtaact ttaaaaaatt atactgatca aaggactgat ccagggttta atatttcaaa 120
aacacagata aatagtttac tacagataaa tagcttcacc c tttggtgtc ctcccagaag 180
catctgaaaa atttctagag ggggtctgtt gaagatgtgt aactagtaca cccaacccc 240
caacctcagt ggaaagcaat gcccagggat taggctatgg aaggggcaaaa tggaccatt 300
caaatttcct cccagggacc aggcctatt aaccctggga aatgtcctta gctggtggg 360
gaaagggttg cgattcagga atacatatgt gtagttttt ttagaagcca tccatagcac 420
acccg
                                         425

```

&lt;210&gt; 375

&lt;211&gt; 478

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(478)

<223> 5' terminal sequence. cd44 antigen (homing  
function and indian blood group system) (CD44)  
gene.

&lt;400&gt; 375

```

ggcgttccag ttcccaattg gaggcenntc atccctcggg tgtgctatgg atggcttcta 60
acaaaaacta cacatatgta ttctgatcg ccaacct ttc cccaccagc taaggacatt 120
tcccagggtt aatagggcct ggtccctggg aggaaatttg aatgggtoca ttttgcctt 180
ccatagccta atccctgggc attgctttcc actgaggttg ggggttggg tgtactagtt 240
acacatcttc aacagacccc ctctangaaa tttttcagat gcttctggga gacacccaaa 300
ggggaagct atttactgt agtaaaactat ttatctgtgt ttttgaaata ttaaacctg 360
gatcagtcct ttgatcagta taaatTTTTT aaagttaactt ttgtcagagg caccaaagg 420
tttaaaactga ttcataaata aatatcngga cttcctcgat cttccaaaaa aaaaaaaa 478

```

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<210> 376  
 <211> 1794  
 <212> DNA/RNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(1794)  
 <223> cd44 antigen (homing function and indian blood group system) (CD44) gene.

<400> 376  
 cccgcgccct ccgttcgctc cggacacccat ggacaagttt tgggtggcag ca gcctgggg 60  
 actctgcctc gtgccgctga gcctggcgca gatcgatttg aatataacct gccgctttgc 120  
 aggtgtattc cacgtggaga aaaatggctg ctacagcatc tctcggacgg aggccgctga 180  
 cctctgcaag gctttcaata gcaccttgcc cacaatggcc cagatggaga aagctctgag 240  
 catcggattt gagacctgca ggtatgggtt c atagaaggg catgtggtga tccccggat 300  
 ccacccaac tccatctgtg cagcaaacaa cacaggggtg tacatcctca catacaacac 360  
 ctccccagat gacacatatt gcttcaatgc ttcagctcca cctgaagaag attgtacatc 420  
 agtcacagac ctgcccattg cctttgatgg accaattacc ataactattg ttaaccgtga 480  
 tggcaccgcg tatgtccaga aaggagaata cagaacgaat cctgaagaca tctaccccag 540  
 caacctact gatgatgacg tgagcagcgg ctccctccagt gaaaggagca gcacttcagg 600  
 aggttacatc ttttacacct tttctactgt acaccccatc ccagacgaag acagtccctg 660  
 gatcaccgac agcacagaca gaatccctgc taccagagac caagacacat t ccaccccag 720  
 tgggggggtcc cataccactc atggatctga atcagatgga cactcacatg ggagtcaaga 780  
 aggtggagca aacacaacct ctggtcctat aaggacaccc caaattccag aatggctgat 840  
 catcttgcca tccctcttgg ccttggtttt gattcttgca gtttgcatg cagtcaacag 900  
 tcgaagaagg tgtgggcaga agaaaaagct agtgatcaac agtggcaatg gagctgtgga 960  
 ggacagaaag ccaagtggac tcaacggaga gccagcaag tctcaggaaa tgggtgcat 1020  
 ggtgaacaag gactcgtcag aaactccaga ccagtttatg acagctgatg agacaaggaa 1080  
 cctgcagaat gtggacatga agattgggtt gtaacaccta caccattatc ttggaaagaa 1140  
 acaaccgttg gaaacataac cattacaggg agctgggaca cttaacagat gcaatgtgct 1200  
 actgattgtt tcattgogaa tcttttttag cataaaattt tctactcttt ttgttttttg 1260  
 tgttttggtc tttaaagtca ggtccaattt gtaaaaacag cattgctttg taaattaggg 1320  
 cccaattaat aatcagcaag aatttgatcg ttcagttcca cttg gaggcc ttcacccctg 1380  
 ggtgtgctat ggatggcttc taacaaaaac tacacatatg tttcctgat cgccaacctt 1440  
 tccccacca gctaaggaca tttcccaggg ttaatagggc ctggtccctg ggaggaaatt 1500  
 tgaatgggtc cattttgccc ttccatagcc taatccctgg gcattgcttt ccactgaggt 1560  
 tgggtgtgac tagttacac a tcttcaacag accccctcta gaaatttttc agatgcttct 1620  
 gggagacacc aaagggtgaa gctatttatc ttagtaaac tatttatctg tgtttttgaa 1680  
 atattaaacc ctggatcagt cctttgatca gtataattt ttaaagttac tttgtcagag 1740  
 gcacaaaagg gtttaaaactg attcataata aatatctgta cttcttcgat cttc 1794

<210> 377  
 <211> 452  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(452)  
 <223> 3' terminal sequence. cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase) (CDKN3) gene.

&lt;400&gt; 377

```
ttttgtcaat aaaacttttag gaatatctgc acatgtacat ttacattcaa gttgataaca 60
ctgggtggtt cattttcaata caaattatgc tagagaactg acatttcaga catgggtcata 120
tatatgctat ttgaattcct ttatcttcga tacagatctt gattgtgaat ctc ttgatga 180
tagatgtgca gctaatttgc cccgaaactc atgaagataa ttgtattgct tgatggctctg 240
tattgccccg gatcctctta ggtctcgca gctgtctatg gcttgctctg gtgatattgt 300
gtcagacagg tatagtagga gacaagcagc tacaagacaa gatctcccaa gtcctccata 360
gcagtgtatt aagggttttc cggtaatttt t aaggcaggt tgtaagcnc tccattattt 420
cacagcagct ggccatgctn ggagtcctcc ca 452
```

&lt;210&gt; 378

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(472)

<223> 5' terminal sequence. cyclin -dependent  
kinase inhibitor 3 (cdk2 -associated dual  
specificity phosphatase) (CDKN3) gene.

&lt;400&gt; 378

```
ggcagcagcg gcaactggtc tcgacgtggg ggggccanga ctgaagccca ngntntcaata 60
caaacaagtg agtttgactc atcagatg aa gagcctattg aagatgaaca gactccaatt 120
catatatcat ggctatcttt gtcacgagtg aattgttctc agtttctcgg tttatgtgct 180
cttccaggtt gtaaattttaa agatgttaga agaaatgtcc aaaaagatac agaagaacta 240
aagagctgtg gtatacaacg acatatttgt tttctgcacc agaggggaac tgtcaaaaata 300
tagagtccca aaccttctgg atctctacca gcaatgtgga attatcacc atcatcatcc 360
aatccgcaga tggagggact cctgacatag ccagctgctg tgaaataatg gaagagctta 420
caacctgcct taaaaattac cgaaaaacct taatacactg ctatggagga ct 472
```

&lt;210&gt; 379

&lt;211&gt; 639

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(639)

<223> cyclin-dependent kinase inhibitor 3  
(cdk2-associated dual specificity phosphatase)  
(CDKN3) gene.

&lt;400&gt; 379

```
atggagccgc ccagttca at acaacaagtg gagtttgact catcagatga agagcctatt 60
gaagatgaac agactccaat tcatatatca tggctatctt tgtcacgagt gaattgttct 120
cagtttctcg gtttatgtgc tcttccaggt tgtaaattta aagatgttag aagaaatgtc 180
caaaaagata cagaagaact aaagagctgt ggtatacaag acatatttgt tttctgcacc 240
agaggggaac tgtcaaaaata tagagtccca aaccttctgg atctctacca gcaatgtgga 300
attatcacc atcatcatcc aatcgcatg ggagggactc ctgacatagc cagctgctgt 360
gaaataatgg aagagcttac aacctgcctt aaaaattacc gaaaaacctt aatacactgc 420
```



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tatggaggac ttgggagatc ttgtcttgta gctgcttgt c tctactata cctgtctgac 480  
acaatatcac cagagcaagc catagacagc ctgcgagacc taagaggatc cggggcaata 540  
cagaccatca agcaatacaa ttatcttcat gagtttcggg acaaattagc tgcacatcta 600  
tcatcaagag attcacaatc aagatctgta tcaagataa 639

&lt;210&gt; 380

&lt;211&gt; 487

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(487)

<223> 5' terminal sequence. max-interacting  
protein 1 (MXI1) gene.

&lt;400&gt; 380

aagtggcgac tggaacagct gcagggtcct caggagatgg aacgaatacg aatggacaga 60  
attggatcaa ctatttcttc agatcggttct gattcagagc gagaggagat tgaagtggat 120  
gttgaaagca cagagttctc ccatggagaa gtggacaata taagtaccac cagcatcagt 180  
gacattgatg accacagcag cctgccgagt attgggagtg acgagggtac tccagtgccca 240  
gtgtcaaaact ttcattcact tcatagaacc cagcatgaca taacagtgcg gggaaaatat 300  
tcaactgggcc attcatataca acaatctctt aaattgggtt catgatgcag tctcctcttt 360  
aaaacaaaac aaaacaaaac aaactatact tgaacaaaag ggtcagagga ctgttttaag 420  
caatacttag caaaagtggg cagctcccaa gagacaattt cagatttcat ttggaaatcc 480  
catttta 487

&lt;210&gt; 381

&lt;211&gt; 2416

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2416)

&lt;223&gt; max-interacting protein 1 (MXI1) gene.

&lt;400&gt; 381

agattatgat cgcttgaggc ccctctccta cccagatacc gatgttatac tgatgtgttt 60  
ttcctttttt tttttttttt ttttaagtaat taagggtagt taaattattt aaagtataca 120  
aagtccaaac agccaggggt aaggtctcca agaggccttc ccagggttaag ggagtgcgga 180  
gaggcccccg tcgccaccg cggtgcccat ggagcgggtg aagatgatca acgtgcagcg 240  
tctgttgag gctgccgagt ttttgagcg ccgggagcga gagtgtgaac atggctacgc 300  
ctcttcattc ccgtccatgc cgagcccccg actgcagcat tcaaagcccc cacggaggtt 360  
gagccgggca cagaacacac gcagcgggac gagcaacacc a gcactgccca acagatctac 420  
acacaatgag ctggaaaaga atcgacgagc tcatctgcgc ctttgtttag aacgcttaaa 480  
agttctgatt ccactaggac cagactgcac ccggcacaca acacttggtt tgctcaacaa 540  
agccaaagca cacatcaaga aacttgaaga agctgaaaga aaaagccagc accagctcga 600  
gaatttgga cgagaacaga gatttttaaa gtggcgactg gaacagctgc agggctccta 660  
ggagatggaa cgaatacga tggacagcat tggatcaact atttcttcag atcgttctga 720  
ttcagagcga gaggagattg aagtggatgt tgaaagcaca gagttctccc atggagaagt 780  
ggacaatata agtaccacca gcatcagtga cattgatgac cacagcagcc tgccgagtat 8 40  
tgggagtgac gagggttact ccagtgccag tgtcaaactt tcattcactt catagaaccc 900

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```

agcatgacat aacagtgcag ggcaaaatat tcactgggcc aattcaatac aaacaatctc 960
ttaaattggg ttcattgatgc agtctcctct ttaaaacaaa aaaaaacaaa aaaaaactat 1020
acttgaacaa aagggtcaga ggacctgtat ttaagcaaa t acttagcaaa aagtggggca 1080
gagctcccaa ggagaacaaa tattcagaat attcatattg gaaaaatcac aatttttaat 1140
ggcagcagaa aacttgtgtg aaattttctt gatttgagtt gattgagaag aggacattgg 1200
agatgccatc ctctttctct tttctcgttt gctcactata cattgagtag acacatttaa 1260
ggatgggggt atgaaccctt cctgagcttt atggtcctaa aagcaaaata aaaactattc 1320
gaatgaaaaa acaagaaaat caggtattaa tcttgatag ctaataatga gctattaaaa 1380
ctcagcctgg gacagtttat catgaagcct gtggatgata aatcctttat tattattttt 1440
tttttttgaa aaaagctcat ttcattgctt gcaaaaggag agactcccat ga agcctttt 1500
gaaagggatc atcatgcagc tcaactttct gttggattcc atgctaagca agctaaccct 1560
atcctgcatt gttagcacta ggcaccagc tgccacctct ccactctgct gcccttaggc 1620
cacatgggag cagtcctatc atgacagcct ctatcctaca aggcctatga gtatggattg 1680
ggggggccaa aaggaaaaag ctccatg tgc ctctttgtct gcgtgggtca gaagagttgt 1740
gcacgcagat tagcaggcca aggtctgagc cacagcagca tttttatttc agattttgat 1800
aactgtttat atgtgttgaa aaccaaaatg acatcttttt aaagcttatc cataaaaaaa 1860
aatagatgtc ttttatagtg gaaaaacaca tggggaaaaa aatcatctat ttgatgcag 1920
catttgataa tgataaaaca cctcacacct cactctttat agtgcacaaa atgaatgagg 1980
tctgggctag gtagaaaaag ggtcaatgct atttttgttt ttagaatcat taccttttac 2040
cagcttttaa ccactctgata tctatagtag acacactatc atagttaaca tagttaagtt 2100
cagcacttgt ctcattttaa tgtaaagatt tgcttccatt ttccctacagg cagtctctct 2160
cttcctcaca gtcccactgt gcaggtgcta ttgttactct tacgaatatt ttcagtaatg 2220
ttattttctt ctaagtgaag tttctagcct gcactttgat gtcattgtgt ccctttgtct 2280
ttcaaactcc aaggttcccc tgtggccctc tcccttacc tggaaggcc tcttgagac 2340
cttaccctg gctgt ttgga ctttgtatac tttaaataat ttaactacc ttaattactt 2400
aaaaaaaaa aaaaaa 2416

```

&lt;210&gt; 382

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(378)

<223> 3' terminal sequence. homeo box a5 (HOXA5)  
gene.

&lt;400&gt; 382

```

tttttttttt ttgttatagt tacttcaagt aacacagctt gttcatata aataagttaa 60
aacatctatt ttttttcaag acaaagccat tcaggacaaa gagatgaaca gaaagcagat 120
ctacttatac aggcgc tata atggcaataa acaggctcat gattaaaaga tgaattaggg 180
caacgagaac agggcttctt cacagaagga acacaaggga gtttcagaaa gtcaccttag 240
tactgacact acgcgggata cgctaaatac tgctcagtag tttaaacgct cagataacta 300
gggacggaag gccctccctt gcccgcgnc atnctccatg gcttttcagc ttattatc tt 360
ttttccactt caatcncc 378

```

&lt;210&gt; 383

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

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<221> misc\_feature  
<222> (1)..(439)  
<223> 5' terminal sequence. homeo box a5 (HOXA5)  
gene.

<400> 383  
aaatcaagca cacatantan aaaacaaatg agctcttatt ttgtaaactc attttgcggt 60  
cgctatccaa atggcccggg ctaccagttg cataattatg gagatcatag ttccgtganc 120  
gagcaattca gggactcggc gagcatgcac tccggcaggt acggctacgg ctacaatggc 180  
atggatctca gcgtcggcng ctcgngctcc ngcacttttg ctccggagag cgcgcccgca 240  
gctacgtnc aagcgcacgc ggcncactcc aagcccaggt acagcnagcc ggccacgtcc 300  
acgcaactcn cctcancng atccgctgcn ctgctccgnc gtnggccctc tcgccngga 360  
ancgacanna ccaanggcgg gaaaaactcc cttaaggca a ctccagcngg cgccctcggg 420  
cgacngccgg aagcaccga 439

<210> 384  
<211> 813  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(813)  
<223> homeo box a5 (HOXA5) gene.

<400> 384  
atgagctctt attttgtaaa ctcatcttgc ggtcgtatc caaatggccc ggactaccag 60  
ttgcataatt atggagatca cagttccgtg agcgagcaat tcagggactc ggcgagcatg 120  
cactccggca ggtacggcta cggctacaat ggcatggatc tcagcgctcg ccgctcgggc 180  
tccggccact ttggctccgg agagcgcgc cgagctacg ctgccagcgc cagcgcggcg 240  
cccgccgagc ccaggtacag ccagccggcc acgtccaagc actctoctca gcccgatccg 300  
ctgccctgct ccgcccgtgc cccctcgccc ggcagcgaca cgcaccacgg cgggaaaaac 360  
tccctaagca actccagcgg cgcctcggcc gacgccggca gc accacat cagcagcaga 420  
gagggggttg gcacggcgtc cggagccgag gaggacgccc ctgccagcag cgagcaggcg 480  
agtgcgcaga gcgagccgag cccggcgcgc cccgcccaac cccagatcta cccctggatg 540  
cgcaagctgc acataagtca tgacaacata ggcgccccgg aaggcaaaag ggcccggacg 600  
gcctacacgc gctaccagac cctggagctg gagaaggagt tccacttcaa ccgttacctg 660  
accgcagaa ggaggattga aatagcaca gctctttgcc tctccgagag acaaattaaa 720  
atctggttcc aaaaccggag aatgaagtgg aaaaaagata ataagctgaa aagcatgagc 780  
atggccgcgg caggaggggc cttccgtccc tga 81 3

<210> 385  
<211> 447  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(447)  
<223> 3' terminal sequence. x-box binding protein  
1 (XBP1) gene.

<400> 385

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```
gcattgtacc ttttaattgc atgggtagtt ttaaataaat ggagaaagca cttttcagaa 60
gctacactag caggaaaaaa ttccatcaag catttacata gtaaatttct ataatttcac 120
aaaagattct tgatcttact tgaagtatac atgagggaaa gagccccctc agcagggtgtt 180
cccgttgctt acagaagcaa actaaaggac ctaaaactgg aggcaagcca ggatgc caaa 240
aagggggaag agaaatgata aagaaccatt cataaattcc atgtctactt caagacattt 300
gtctaatac ctttacataa taagtatttt agggaaaact accacccttt taagataaaa 360
gtacaatctt aaaagctgta gttctcaatt atagtaatat ttcntacttc cagtaatatg 420
tctcaatacc ttggactgct ggatgtc 447
```

&lt;210&gt; 386

&lt;211&gt; 462

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(462)

&lt;223&gt; 5' terminal sequence. x-box binding protein

1 (XBP1) gene.

&lt;400&gt; 386

```
aagaacctgt agaagatgac ctcggtccgg agctgggtat ctcaaactctg ctttcatcca 60
gccactgccc aaagccatct tcctgcctac tggatgctta cagtgaactgt ggatacgggg 120
gttccctttc cccattcagt gacatgtcct ctctgcttgg tgtaaaccat tcttgggagg 180
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tctcatagat gacccccagg tattgtcttt tgacatccca agcagtccaa ggtattggag 420
acatattact gggaagtaaa gaaatattac tnataattgg ag 462
```

&lt;210&gt; 387

&lt;211&gt; 1836

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1836)

&lt;223&gt; x-box binding protein 1 (XBP1) gene.

&lt;400&gt; 387

```
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aacatctccc catggattct ggcggtattg actcttcaga ttcagagtct gatatcctgt 660
tgggcattct ggacaacttg gaccagtcga tgttcttcaa atgcccttcc ccagagcctg 720
```

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ccagcctgga ggagctccca gaggtotacc cagaaggacc cagttcctta ccagcctccc 780
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caattaaaag gtacaatgca aaaaaaaaa aaaaaa 1836

```

&lt;210&gt; 388

&lt;211&gt; 433

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(433)

<223> 3' terminal sequence. tumor necrosis factor,  
alpha-induced protein 3 (TNFAIP3) gene.

&lt;400&gt; 388

```

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aaatttcaaa tactttttat aataagtata aataattact ttttttcaca ttaagaatgg 180
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gaagtttatt tngtatctct tggaangaa ttataaagat tcgtctggga aaaactt agg 300
gggctctaag gggaaagttg tgcctaatag tatgagtaaa ggctgtgtag agttatggat 360
cacaaatatt ttcaggcont aagtacagac ccccnaaatg gcagccttta tcncggggga 420
aatgcattt ccc 433

```

&lt;210&gt; 389

&lt;211&gt; 206

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(206)

<223> 5' terminal sequence. tumor necrosis factor,  
alpha-induced protein 3 (TNFAIP3) gene.

&lt;400&gt; 389

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```
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ttttattaca aacttcaaga ttatttaagt gaagatattt cttcagctct ggggaaaatg 120
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ccacagggag taaatngnn cctctt 206
```

&lt;210&gt; 390

&lt;211&gt; 4426

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4426)

<223> tumor necrosis factor, alpha -induced protein  
3 (TNFAIP3) gene.

&lt;400&gt; 390

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agcacaatgg ctgaacaagt ccttctcag gctttgtatt tgagcaatat gcggaaagct 120
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cattttaaaa ccattgcaccg atacacactg gaaatgttca gaacttgcca gtt ttgtcct 240
cagtttcggg agatcatcca caaagccctc atcgacagaa acatccaggc caccctggaa 300
agccagaaga aactcaactg gtgtcgagaa gtccggaagc ttgtggcgct gaaaacgaac 360
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&lt;210&gt; 391

&lt;211&gt; 440

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(440)

<223> 3' terminal sequence. serum response factor  
(c-fos serum response element-binding  
transcription factor) (SRF) gene.

&lt;400&gt; 391

```

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aacacacatt ataagcactt tgcctgattc actcactnng gtctgtcttt tgtgggaagg 360
agagggaaga ttcatcaaag gtctcctccc catgggtngg gggagtgggg agtgagttag 420
tgatggtgga gtgaaacaag

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<210> 392  
<211> 471  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(471)  
<223> 5' terminal sequence. serum response factor  
(c-fos serum response element-binding  
transcription factor) (SRF) gene.

<400> 392  
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atgggggaag attttaatgc acagccta gt tatcaagggg atgatttgcc g 471

<210> 393  
<211> 4201  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(4201)  
<223> serum response factor (c-fos serum response  
element-binding transcription factor) (SRF) gene.

<400> 393  
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tatttttatg tgcagcgacc cttgggtgtt cccttctcg gtgctctgg ggtatgtgtg 4020
tgtgggtgtg tgcgcctgag tgagtgtgtg tgagtgtgta tgct agtgg 4080
ttctacttcc cctgggatgc tgaccagga atagtggaca tggtcacagt cctatgtaca 4140
gagctttctt ttgtattaaa aaaaaatact ctttcaataa atgtatcatt tttgtgcaca 4200
g 4201

```

&lt;210&gt; 394

&lt;211&gt; 563

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(563)  
<223> 3' terminal sequence. sry (sex determining  
region y)-box 9 (campomelic dysplasia, autosomal  
sex-reversal) (SOX9) gene.

<400> 394  
tttttaaatgc aatgtatatatt tattgtaaac aataatatac aaaaaaaaaa aagagaaaga 60  
aaaagggaaa ggtaagtttc acggagagaa caaaagggttt ggggctggga gggaaacaag 120  
tgaacaaac aaaacacgaa cacaaccaa agcttttacc taaagacaaa atatgattta 180  
aatgccaggt ttcttaagtt acaga agtat ctttttaaaa agatctgctt ttatacagaa 240  
attgaaggat gccatattat gagtgtttta agattttatt ctactgactt ctaaaactgt 300  
taatatatct ttttttaaat aaaaaaaaaa gtttgctgtc ttttttaaaa agcaatcctc 360  
aaactctcta gccacagcag taattaagat taagggtctgt cagtgggctg atcccctcca 420  
ggtagcctcc ctactccaa gagaagatgc ngagaaatat gggatggaca catgcctgca 480  
tgtttttgtg nccaaacaca cacanacca nacacacnca caatataagg cngccccaag 540  
gtctntggcc gaaancctgg caa 563

<210> 395  
<211> 3936  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3936)  
<223> sry (sex determining region y) -box 9  
(campomelic dysplasia, autosomal sex -reversal)  
(SOX9) gene.

<400> 395  
ggagagccga aagcggagct cgaaactgac tggaaacttc agtggcgcgagg agactcgcca 60  
gtttcaacc cggaactttt tctttgcagg aggagaagag aaggggtgca agcgcccca 120  
cttttgctct ttttctctcc ctctctctcc tctocaattc gctcccccc acttgagcgg 180  
ggcagctgtg aactggccac ccgcgcctt cctaagtgtc cgccgcggta gccggc cgac 240  
gcgccagctt ccccgaggc cgcttgcctc gcatccgggc agccgagggg agaggagccc 300  
gcgcctcgag tcccagagcc gccgcggctt ctgcctttc ccggccacca gcccctgcc 360  
ccgggcccgc gtatgaatct cctggacccc ttcatgaaga tgaccgacga gcaggagaag 420  
ggcctgtccg gcgccccag cccaccatg tccg aggaact ccgcgggctc gccctgcccg 480  
tcgggctccg gctcggacac cgagaacacg cggccccagg agaacacgtt cccaagggc 540  
gagcccgatc tgaagaagga gacgaggag gacaagttcc ccgtgtgcat ccgcgaggcg 600  
gtcagccagg tgctcaaagg ctacgactgg acgtgtgtgc ccatgccggt gcgcgtcaac 660  
ggctccagca agaacaagcc gcacgtcaag cggcccatga acgccttcat ggtgtgggag 720  
caggcggcgc gcaggaagct cgcggaccag taccgcact tgcacaacgc cgagctcagc 780  
aagacgctgg gcaagctctg gagacttctg aacgagagcg agaagcggcc cttcgtggag 840  
gaggcggagc ggctgcgcgt gcagcacaag aaggaccacc cggattacaa gtac cagccg 900  
cggcggagga gtcggtgaa gaacgggagc gcggaggcag aggaggccac ggagcagacg 960  
cacatctccc ccaagccat ctcaaggcg ctgcaggccg actcgccaca ctctcctcc 1020  
ggcatgagcg aggtgcactc ccccggcgag cactcggggc aatcccaggg cccaccgacc 1080  
ccaccacca ccccaaaac cgacgtgcag ccgggcaagg ctgacctgaa gcgagagggg 1140  
cgcccttgcc cagagggggg cagacagccc cctatcgact tccgcgacgt ggacatcggc 1200  
gagctgagca gcgacgtcat ctccaacatc gagaccttcg atgtcaacga gtttgaccag 1260  
tacctgccgc ccaacggcca cccgggggtg ccggccacgc acggccaggc cacctacacg 1320  
ggcagctacg gcatcagcag caccgcgcc acccggcga gcgcgggcca cgtgtggatg 1380  
tccaagcagc aggcgcgcgc gccaccccc cagcagcccc cacaggcccc gccggccccg 1440

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caggcgcccc cgcagccgca ggcggcgccc ccacagcagc cggcggcacc cccgcagcag 1500
ccacagggcg acacgctgac cagcgtgagc agcagcgccg gccg gtccca gcgaacgcac 1560
atcaagacgg agcagctgag cccagccac tacagcgagc agcagcagca ctgcgcccaa 1620
cagatcgct acagccctt caacctccca cactacagcc cctcctacc gcccatcacc 1680
cgctcacagt acgactacac cgaccaccag aactccagct cctactacag ccacgcggca 1740
ggccagggca cggcctct a ctccacctt acctacatga acccgtctca gcgccccatg 1800
tacaccccca tcgcccacac ctctggggtc ccttccatcc cgcagacca cagccccag 1860
cactgggaac aaccgctcta cacacagctc actcgacctt gaggaggcct cccacgaagg 1920
gcgacgatgg ccgagatgat cctaaaaata accgaagaaa gagaggacca accagaat tc 1980
cctttggaca tttgtgttt tttgttttt tattttgtt tgttttttct tcttcttctt 2040
cttcttaaa gacatttaag ctaaaggcaa ctgtaccca aatttccaag acacaaacat 2100
gacctatcca agcgatttac ccacttgttg ccaatcagtg gccaggccaa ccttggctaa 2160
atggagcagc gaaatcaacg agaaactgga ct ttttaaac cctcttcaga gcaagcgttg 2220
aggatgatgg agaatcggt gatcagtggt ctaaattctt ctgcctgtt ggactttgt 2280
attattttt tagcagtaat taaagaaaa agtcctctgt gaggaatatt ctctatttta 2340
aatattttta gtatgtactg tgtatgattc attaccattt tgaggggatt tatacatatt 2400
tttagataaa attaaatgct cttatttttc caacagctaa actactctta gttgaacagt 2460
gtgccctagc tttcttgca accagagtat tttgtacag atttgcttcc tcttacaaaa 2520
agaaaaaaa aatcctgttg tattaacatt taaaaacaga attgtgttat gtgatcagtt 2580
ttgggggtta actttgctta attcctcagg ctttgcgatt taagga ggag ctgccttaaa 2640
aaaaataaa ggccttattt tgcaattatg ggagtaaaca atagtctaga gaagcatttg 2700
gtaagcttta tgatatatat attttttaa gaagagaaaa acaccttgag ccttaaaaacg 2760
gtgctgctgg gaaacatttg cactctttta gtgcatttcc tcctgccttt gcttgttcac 2820
tgcagtctta agaaagaggt aaaaggcaag caaaggagat gaaatctgtt ctgggaatgt 2880
ttcagcagcc aataagtgcc cgagcacact gccccgggt gcctgcctgg gcccatgtg 2940
gaaggcagat gcctgctgc tctgtcacct gtgcctctca gaacaccagc agttaacctt 3000
caagacatto cacttgctaa aattatttat tttgtaagga gaggttttaa ttaaaacaaa 3060
aaaaaattct tttttttt tttttttcca attttacctt ctttaaaata ggttgttga 3120
gctttcctca aagggtatgg tcatctgttg ttaaattatg ttcttaactg taaccagttt 3180
ttttttattt atctctttaa tcttttttat tattaaaagc aagtttcttt gtattcctca 3240
ccctagattt gtataaatgc cttttgttcc atcc cttttt tctttgttgt tttgttgaa 3300
aacaaactgg aaactgttt cttttttgt ataaatgaga gattgcaaat gtagtgtatc 3360
actgagtcac ttgcagtgtt ttctgccaca gacctttgg ctgccttata ttgtgttgt 3420
gtgtgggtgt gtgtgtgtt tgacacaaaa acaatgcaag catgtgtcat ccatatttct 3480
ctacatcttc tcttgagtg agggaggcta cctggagggg atcagcccac tgacagacct 3540
taatcttaat tactgtgtg gctagagagt ttgaggattg ctttttaaaa aagacagcaa 3600
actttttttt ttatttaaaa aaagatatat taacagtttt agaagtcagt agaataaaat 3660
cttaaaagcac tcataatatg gcaccttca attctgtat aaaagcag at ctttttaaaa 3720
aagatacttc tgtaacttaa gaaacctggc atttaaatca tattttgtct ttaggtaaaa 3780
gctttgggtt gtgttcgtgt tttgtttgt tcaattgttt cctcccagc cccaaacctt 3840
ttgttctctc cgtgaaactt accttcctt ttttcttct cttttttttt ttgtatatta 3900
ttgtttacaa taaatatata tt gcattaaa aagaaa 3936

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&lt;210&gt; 396

&lt;211&gt; 204

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(204)

<223> 3' terminal sequence. cadherin 15,  
m-cadherin (myotubule) (CDH15) gene.

&lt;400&gt; 396

```

tttttttttt tttttttttt tttttttttt ttttttttca ttcagattta cccaggaggt 60
tgctgtcttt canacaaaga tgagggtcac tgnnaggagg caaagggtggg actaggagg 120

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tgacccgcat gggccagatn ggagagaaac tcttcccacc ccggcagaag gggcctcttc 180  
ctggccgccc catccanact cagg 204

&lt;210&gt; 397

&lt;211&gt; 458

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(458)

<223> 5' terminal sequence. cadhe rin 15,  
m-cadherin (myotubule) (CDH15) gene.

&lt;400&gt; 397

caggacgcct acgacatcag ccagctgcgt caccgcagag cgctgagcct gcctctggga 60  
ccgcgcgccac ttccgagaga tgcccgcag ncagcctgca ccccagcca ccccgagtgc 120  
tgcccaccag cccctggac atcgccgact tcatcaatga tggcttga g gctgcagata 180  
gtgacccag tgtgcgcct tacgacacag ccctcatcta tgactacgag ggtgacggct 240  
cgggtggcggg gacntgagct ccctcctgtc cagccagggc gatgaggacc aggactacga 300  
ctacctcaga gactgggggc cccgcttcgc ccggctggca gacatgtatg ggcacccgtg 360  
cgggttngga gttacggggc cagatgg gac caccaggcca gggagggctt ttctcctggg 420  
gcactgctac ccagacacag aggcgggaca gcctgan 458

&lt;210&gt; 398

&lt;211&gt; 2833

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2833)

<223> cadherin 15, m-cadherin (myotubule) (CDH15)  
gene.

&lt;400&gt; 398

acttgcgctg tactcagcc tggacgcgt tcttcgggtc gggggtgcac tccggcccg 60  
ctcccgcctc ggcccgatg gacgcgcgt tctcctcgt cctcgggctg ttggcccaga 120  
gcctctgcct gtctttggg gtt cctggat ggaggaggcc caccacctg taccctggc 180  
gccgggcgcc tgccctgagc cgcgtgcga gggcctgggt catcccccg atcagcgtat 240  
ccgagaacca caagcgtctc ccctacccc tgggttcagat caagtcggac aagcagcagc 300  
tgggcagcgt catctacagc atccaggac ccggcgtgga tgaggagccc cggggcgtct 360  
tctctatcga caagttcaca gggaaggtct tctcaatgc catgctggac cgcgagaaga 420  
ctgatcgtt caggctaaga gcgtttgcc tggacctggg aggatccacc ctggaggacc 480  
ccacggacct ggagattgta gttgtggatc agaatgacaa ccggccagcc ttcctgcagg 540  
aggcgttcac tggccgcgtg ctggagggtg cagtcccagg cac ctatgtg accagggcag 600  
aggccacaga tgccgacag cccgagacg acaacgcagc gctgcggtc tccatcctgc 660  
agcagggcag ccccgagctc ttcagcatc agagagatc cgcacagtgc 720  
aagtggggct ggaccgcgag gtggtgcggt tgtacaatct gaccctgcag gtggcggaca 780  
tgtctggaga cggcctcaca g cactgcct cagccatcat cacccttgat gacatcaatg 840  
acaatgcccc cgagttcacc agggatgagt tcttcatgga ggccatagag gccgtcagcg 900  
gagtggatgt ggagcgcctg gaagtggagg acagggacct gccaggctcc ccaaactggg 960  
tggccagggt caccatcctg gaaggcgacc ccgatgggca gttcaccatc cgcacggacc 102 0

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ccaagaccaa cgagggtgtt ctgtccattg tgaaggccct ggactatgag agctgtgaac 1080
actacgaact caaagtgtcg gtgcagaatg agggcccgct gcaggcggct gcccttaggg 1140
ctgagcgggg ccaggccaag gtccgcgtgc atgtgcagga caccaacgag ccccccgtgt 1200
tccaggagaa cccacttcgg accagcctag cagagggg gc acccccaggg actctggtgg 1260
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gccagggtcaa cgtgagccac gcgcgcctgc ggccgcgaca ccaggtcccc gaaggcctgc 1740
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ccttctctgc ggggtgggaa gagtttctct ccacggccc catgcgggtc acc tccctag 2760
tccaccttt gcctctacc agtgaacctc atctttgtat gaaagacagc aacctcctgg 2820
gtaaatctga atg 2833

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&lt;210&gt; 399

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(646)

<223> 3' terminal sequence. b-cell cll/lymphoma 2  
(BCL2) gene.

&lt;400&gt; 399

```

tatctcacac tgtactttat tttcttcac aatattaact agacagacaa ggaaagtta 60
atggcaatgt gactttttcc aacaacacaa acaaagtgcc attata gcta atggtggcca 120
actggagact tactttacct taacctatga aagtatcctt accgtatttt ttatgtgtac 180
agtgttgtag aatatcagcc acctcttaaa agtatcaatc ttaaaaagag ccatggaagg 240
taaaagtatg aaaatcttga taacaaaagc tttaataca aaaacactta ttgtacactt 300
atttttattt aaacaaaaaa taac ccagat aactcaaaac aaaagcaaac cttggttgaa 360
aacttaagaa ggtataataa acaaaaccac caaaagaaag cttcccaaaa agaaatgcaa 420
tccactgtca ctcttgcaaa ttctaccttg gagggaaaaa cttaatgaaa tgagctatct 480
ggaggggcca cggagatttt ccaaaagggt taggtgcatg gatttactca gtatctacnt 540
acagtcttat ttattaatag ctgaganttc ctgattgagc gagcctttcc atctccacca 600
gtgtcccccac ttctgtgcnc acttgggntg cagacaccct gtgttg 646

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<210> 400  
<211> 465  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(465)  
<223> 5' terminal sequence. b-cell cll/lymphoma 2  
(BCL2) gene.

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ttggtaggga catctgtttc taaatgttta ttatgtacaa tacagaaaaa aattttataa 1 20  
aattaagcaa tgtgaaactg aattggagag tgataataca agtccttttag tcttaccag 180  
tgaatcattc tgttccatgt ctttggacaa ccatgacctt ggacaatcat gaaatatgca 240  
tctcactgga tgcaaagaaa atcagatgga gcatgaatgg tactgtaccg gttcatctgg 300  
actgccccag aaaaaaact tcaagcaaac atcctatcaa caacaagggt gttctgcata 360  
ccaagctgag cacagaagat gggaacactg gtggaggatg gaaaggctcg ctcaatcaag 420  
aaaattctga gactattaat aaataagact gtagtgtaga tactg 465

<210> 401  
<211> 419  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(419)  
<223> 3' terminal sequence. ests (EST W73386)  
gene.

<400> 401  
gaaggtcatt cttgcgatgg gtttattgca ggagatgatg gaccaaattg ctctgacaca 60  
tgcacacgct cctgggcacg cctgctgcgn gtncgcttcc catga cccc agggccctct 120  
atgcctcccc cccagggcac cctgcccact tgccccact tcatgtacca ccaagccctt 180  
tccttttctg ggcaccactc ctgagcagcg tgaccagcgg cctccaagtg catgtggctc 240  
agaacataaa agcatcttca acattcgtca ttgagccaaa cgaaacacag tgtttggtc 300  
aagagccggc gacactngca tcc ctatcca cactgtgaac ctgcccttgg gcttngttga 360  
ccggaggatn ggccgctctt ccttgtcatc cagcancgg agcatgtatg tgcccaga 419

<210> 402  
<211> 568  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(568)  
<223> 3' terminal sequence. granzyme a (granzyme

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1, cytotoxic t-lymphocyte-associated serine  
esterase 3) (GZMA) gene.

&lt;400&gt; 402

```
tcatgcaaat tgattttatt tgtgaaaaga ttaagaagcc acagtanatg aaaggaaacg 60
gttattttaa ctgctccctt gatagt cata attatccagt tgagggtgtt ctttgagaga 120
agaatataga caccaggccc acgagggtct ccgcatttat tttcaaggcc aaaggaagtg 180
accctcgga aaacaccctc gcacaacaaa gggcttccag aatctccatt gcacgagtct 240
cttccacctc ggaggcttcc agcacaaccc atattcattc caatcacagg gttaaaatta 300
tagtgatttc gatcattgca gacttttctg tctatgatgg gtgatattga cttgactca 360
gagtatcggg acccaagatg cactattggg gagtcctgcc ccaccctggc aacttggcac 420
atggttctct gntttcacat caatccccct ttttagggag atgaaggata gtcacatain 480
tggtnathtt ggctttttcc ggtcagctgt aaagttttta ggtccc ctnc gcgtttggtg 540
gggcctagcc tgggagggga aanccttt 568
```

&lt;210&gt; 403

&lt;211&gt; 878

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(878)

<223> granzyme a (granzyme 1, cytotoxic  
t-lymphocyte-associated serine esterase 3) (GZMA)  
gene.

&lt;400&gt; 403

```
cagattttca ggttgattga tgtgggacag cagccacaat gaggaactcc tatagatttc 60
tggcatcctc tctctcagtt gtcgtttctc tcctgctaatt tcctgaagat gtctgtgaaa 120
aaattattgg aggaaatgaa gtaactcctc attcaagacc ctacatggtc ctacttagtc 180
ttgacagaaa aaccatctgt gctggggctt tgattgcaaa agactgggtg ttgactgcag 240
ctcactgtaa cttgaacaaa aggtcccagg tcattcttgg ggctcactca ataaccaggg 300
aagagccaac aaaacagata atgcttggtta agaaagagt tcc ctatcca tgctatgacc 360
cagccacacg cgaagggtgac cttaaacttt tacagctgac ggaaaaagca aaaattaaca 420
aatatgtgac tatccttcat ctacctaaaa agggggatga tgtgaaacca ggaaccatgt 480
gccaagttgc aggtgggggg aggaactaca atagtgcac ttgggtccgat actctgagag 540
aagtcfaatc caccatcata gacagaaaag tctgcaatga tcgaaatcac tataatttta 600
accctgtgat tggaaatgaat atggtttgtg ctggaagcct ccgaggtgga agagactcgt 660
gcaatggaga ttctggaagc cctttgttgt gcgagggtgt tttccgagg gtcacttctc 720
ttggccttga aaataaatgc ggagaccctc gtgggccttg tgtctatatt cttctctcaa 780
agaaacacct caactggata attatgacta tcaagggagc agtttaaata accgtttcct 840
ttcattttact gtggcttctt aatcttttca caaataaa 878
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&lt;210&gt; 404

&lt;211&gt; 191

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(191)

&lt;223&gt; 3' terminal sequence. v-fos fbj murine

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osteosarcoma viral oncogene homolog (FOS) gene.

&lt;400&gt; 404

```
gcagtgaccg tgctcctacc cagctctgct tcacagcgcc cacctgtctc cgcccctcgg 60
ccccctgccc ggctttgcta accgccacga t gatgttctc gggcttcaac gcagactacg 120
aggcgtcatc ctcccgtgc agcagcgct ccccgccgg gataanctct ctttattaca 180
attaatcanc g 191
```

&lt;210&gt; 405

&lt;211&gt; 245

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(245)

<223> 5' terminal sequence. v-fos fbj murine  
osteosarcoma viral oncogene homolog (FOS) gene.

&lt;400&gt; 405

```
ttttcaactt aaatgctttt attgacaatg tcttgaaca ataagcaaac aatgcttaaa 60
tttttcattc aaattcactt tccacatgtc aaaagacctc aaggtagaaa aaaataaaat 120
aaaaatataa atatctgaga atccatctta ataaataaat taaaaacaca ataaaacgtt 180
tcatggaaa actgttaatg tccngaacat tcagaccacc tcnacaatgn gtgntongtn 240
anatt 245
```

&lt;210&gt; 406

&lt;211&gt; 489

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(489)

<223> 3' terminal sequence. interleukin enhancer  
binding factor 1 (ILF1) gene.

&lt;400&gt; 406

```
gcgncgcgct caccgaagg gngangtaga cagcgggtca gaggccgcct agagccggag 60
gacaccccaa atacaaacat accacggaga gacctgggat ctgagtttca aaagggcctg 120
tgataaaaga ctgaatcttt ttccaaatga agtagaaatg gttctgtcgt tttaaacata 180
cacaatactt aggagacttg tt ttactcag agtggaat tttgccaggg acaaagtcaa 240
cacaagaaaa caaacaacaa aaaatagcca gaaagagaac agttaagtgc agtcgggtga 300
gtcccggcag ttccctcccg gcaactggctc gtccctgggt tctcaagggt ccatgcggcc 360
acagcgtccg tccacctgtc cagcggagcc acatgtctgaa atgggaggtg ggataaaatt 420
catcaggcag ctgctgtaac acggaaatgt gcagatgcc a gtagcttc gtctgaactt 480
gaacaagac 489
```

&lt;210&gt; 407

&lt;211&gt; 247

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(247)  
<223> 5' terminal sequence. interleukin enhancer  
binding factor 1 (ILF1) gene.

<400> 407  
tggtttcagc ctatggaatg atttcctttt gtctgtcttg ttcaagttca gacgaagcta 60  
ctctggcatc tgcacatttc cgtgttacag cagctgcctg atgaa tttta tccacctcca 120  
tttcagcatg tggctcgcgt ggacaggtgg acggacgctg tggccgcatg gaaccttgag 180  
aaccaggga cgagccagtg ccgggaagga actgccggga ctaccganc tgcncttaac 240  
tggtctc 247

<210> 408  
<211> 3059  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3059)  
<223> interleukin enhancer binding factor 1 (ILF1)  
gene.

<400> 408  
gcccccccc cagcctcct cccctcctcc cgcccgcgcg tgctcccgcc cctcgccgcc 60  
gtctgctcgc tcgcccgcgc gcctccgctc ggccccctcc ctacagctccg gtgcgcggcg 120  
gccgacgacc cgcggccttg gcctcggcgc gccaccggcg ccgcgcgga gcggcccggg 180  
ggccctcagc caggcccatg gcggcggcgc gcgcgctct cgggcgggc accacgcggg 240  
cgcgggggcg ggggcgcgg ggcggggcg ggtcccgccg ggcgctgggc cgtggggcgc 300  
ctggagggcc gcgagtga gtatctgat aagaagcgt cggtagccat cggccgcaac 360  
tcgtcgcagg gctcgttgga cgtgagcat gccactcga gcttcattc cggcgccac 420  
ctcgagatct tcacgcccc gggcgcgcg gccatggcg ggcgctccg gagctgccgc 480  
ccgcgcagcc caggcccgac gccggcgcg acttctacct gcgctgcttg ggcaagaacg 540  
gggtattcgt ggacggcgtg ttccagagg gcggggcgcc gccgctgcag ctgccgcgcg 600  
tgtgcacatt caggttcccg agcacaaca tcaagataac gttcactgcc ctgtccagcg 660  
agaagagaga gaagcaggag gcgtctgagt ctccagtga a ggccgtacag ccacacatct 720  
cgccctgac catcaacatt ccagacacca tggcccacct catcagccct ctgccctccc 780  
ccacgggaac catcagcgt gcaaactcct gccctccag ccccgggga gcgggggtctt 840  
cagggtacaa ggtgggccga gtgatgccat ctgacctcaa tttaatggct gacaactcac 900  
agcctgaaaa tgaaaag gaa gcttcagggt gagacagccc gaaggatgat tcaaagccgc 960  
cttactccta cgcgcagctg atagttcagg cgattacgat ggctcccgac aaacagctca 1020  
ccctgaacgg gatttataca cacatcacta aaaattatcc ctactacagg actgcggaca 1080  
agggctggca gaattcaatt cgcacaatc tctctctgaa tcgttatttc atcaaag tgc 1140  
cgcgttccca ggaagaacca ggcaaaggct cgttctggag gatagacca gcctctgaaa 1200  
gcaaattaat agaacaagg tttaggaac gcggcctag gggcgctgcc tgcttttagaa 1260  
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agcggcagct accacaggcc atcaagcctg tcacctacac tgtggccacc ccagtgacca 1560  
cctcgacctc ccagccaccc gtcgtgcaga cgttcacgt cgteccaccg atcccagcgg 1620  
tgtcggtcac cagtgtggcc ggactggccc cagcgaacac gtacactgtc tctggacaag 1680

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```
ctgtggtcac cccggcagcc gtgctggccc ctccaaagc agaggcccag gagaatggag 1740
accacagga agtcaaagt aaagtagagc ctattcccgc cattg gccac gccacgctcg 1800
gcaactgcc cgggatcatt cagacggcac agaccacccc ggtccagacg gtgaccatag 1860
tacaacagga acctctaggt caacaccagc taccaataaa aactgtaaca caaacggca 1920
ctcacgtggc atcagtcacc actgcggtcc acggccaggt gaacaatgcc gcggcgagtc 1980
ctttgcacat gttggcaaca cagcatocg catcgccctc cctgcccaca aagcgccaca 2040
acggtgacca gccggagcag ccggagctga agcgatcaa gacagaagac ggcgaggcca 2100
tcgtcattgc cctgagcgtg gacacgccac cggcagccgt aagggaaaag ggtgtccaga 2160
actagcgacc gggagagctt ttctttaacg atatcaactc tgtggtgcca aaaggagac g 2220
cggcctcccg ccagcactcg ggggtgcagg gccctgtggt tggacttcac ctctcagcac 2280
tgaaaaccca aaacccagct ggccttaaca ctccctaaag acagaagtca cacttgaaca 2340
aaacccacac acaacaaaac ctgatttggg agacggtgtc tccactgagc acctgctggg 2400
ctgagcttct acctacgagt gaaactctgt cct ccgcga ggaccaggca tcgctgtgtg 2460
aggacggcac gccagcgcg tgctgtgagt gggctctcca agactaggcc tcaggacgcg 2520
gggggagcca tccccgcgc cctcacagga cccaccaggc agcggagaca tgtggaatta 2580
gagtattttg aggtgtcctt tctttacaaa ataatggggt cttgggcatt tcacatcact 2640
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ttgttcaagt tcagacgaag ctactctggc atctgcacat ttccgtgtta cagcagctgc 2820
ctgatgaatt ttatccacct ccatttcagc atgtggctcg cgtggac agg tggacggacg 2880
ctgtggccgc atggaacctt gagaacccag ggacgagcca gtgccgggaa ggaactgccg 2940
ggactcaccg agctgcactt aactgttctc tttctggcta tttttgttg tttgttctt 3000
tgtgttgact ttgtccctgg caaaatttct cactctgagt aaaacaagtc tcggaattc 3059
```

&lt;210&gt; 409

&lt;211&gt; 201

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(201)

<223> 3' terminal sequence. rho gdp dissociation  
inhibitor (gdi) alpha (ARHGDIA) gene.

&lt;400&gt; 409

```
tttttttttt tccttcaggg gcatttattt cccggtcaga aaagaagcag ggacaggcgc 60
ctctgcctga gcttggcaga cacaacacga agaccgggga tggggcgggg gaggcacagg 120
agacggctct cagcaatgtg tgcacttggt cccttggttg ttcttggtg ggtcagggaa 180
ggcctgccgn ggggtggtggc a 201
```

&lt;210&gt; 410

&lt;211&gt; 297

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(297)

<223> 5' terminal sequence. rho gdp dissociation  
inhibitor (gdi) alpha (ARHGDIA) gene.

&lt;400&gt; 410

258/292

ggcctctgct gccctttctg tgccccccag gttctatctc cccgtcacac ccgaggcctg 60  
gcttcaggag ggagcggana gccattctcc agggcccggtg gttgccctg gacgtgtgcg 120  
tctgctgctc cggggtggan ctgggtgtg ggatgcacgg cctcgtggg gccgggccgt 180  
cctccagccc cgtgctccc tggccagccc cc ttgtcgt gtcggtccc tctaaccatg 240  
atgccttaac atgtggagtg tacctgtggg gcctcactaa gcctctaant cactgtg 297

&lt;210&gt; 411

&lt;211&gt; 1819

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1819)

<223> rho gdp dissociation inhibitor (gdi) alpha  
(ARHGDI A) gene.

&lt;400&gt; 411

cctgaaccgc gcggccgaac cctccgggtg cccgaccag gctaagcttg agcatggctg 60  
agcaggagcc cacagccgag cagctggccc agattgcagc ggagaacgag gaggatgagc 120  
actcgtcaa ctacaagccc ccggcccaga agagcatcca ggagatccag gagctggaca 180  
aggacgacga gagcctgcga aagtacaagg aggcctgct gggccgcgtg gccgtttccg 240  
cagaccccaa cgtcccaaac gtctgtgtga ctggcctgac cctggtgtgc agctcggccc 300  
cgggcccccct ggagctggac ctgacgggag acctggagag cttcaagaag cagtcgtttg 36 0  
tgctgaagga ggggtgtggag taccggataa aaatctcttt ccgggttaac cgagagatag 420  
tgtccggcat gaagtacatc cagcatacgt acaggaaagg cgtcaagatt gacaagactg 480  
actacatggt aggcagctat gggccccggg ccgaggagta cgagttcctg acccccgtgg 540  
aggaggcacc caagggtagt ctggccccgg gcagctacag catcaagtcc cgcttcacag 600  
acgacgacaa gaccgaccac ctgtcctggg agtggaaatc caccatcaag aaggactgga 660  
aggactgagc ccagccagag gcgggcaggg cagagtgtat gacggaagac ggacaggcgg 720  
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cctccaccct ggtccgcct c cctggcctgg ctcaaccgag tgccctccgac cccctcctc 840  
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tgtgtgtggt gggagagagg ccgagccag gcctctgctg ccctttctgt gccccccagg 960  
ttctatctcc ccgtcacacc cgaggcctgg cttcaggagg gagcggagca gccattctcc 1020  
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ccttgtcgtg gtcggtccc tctaaccatg atgccttaac atgtggagtg taccgtgggg 1200  
cctcactagc ctctactccc tgtgtctgca tgagc atgtg gcctccccgt ccctccccg 1260  
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ggggaagcga aaattgccaa cactcaagtc acctcagtag catccaggag gctgggtatt 1440  
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ccctcgatgg acaggcctga cccacccac ctggggccag ccaggagccc cgcctgggcc 1560  
atcagtatct attgcctccg tccgtgccgt ccctgggcca ctggctggcg cctcttccc 1620  
cagcctctca gtgccaccac cccggcagc ctccctgac ccagccagg a caaacaagg 1680  
accaagtgc cacttgctg agagccgtct cctataggtc ccccgccca tccccgtgt 1740  
tggtgtgtg tctgccaggc tcaggcagag gcgcctgtcc ctgcttcttt tctgaccggg 1800  
aaataaatgc ccctgaagg 1819

&lt;210&gt; 412

&lt;211&gt; 306

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

259/292

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(306)

<223> 3' terminal sequence. complement component  
4a (C4A) gene.

&lt;400&gt; 412

```
gctgccaaaa gcctttaata tgccctggtc ccaggctgt g ttcattgaaag cggacacagc 60
agtgtctcca gcttcatggt tcccagggtc aggttctctc cagcggaggt gggagggcag 120
ccctcacacc tggcaccctt gattgcatac tcttgaggga agtcgttgag ctggggcacag 180
gctgcccgtt ggcgggttgcn tccggcacag gcgttcagag ggcattctct cgatccagct 240
attcgagtcc agcaagta ct ngggggggnc cctcccaggg gcataantng gncntccag 300
anccat
```

&lt;210&gt; 413

&lt;211&gt; 5417

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(5417)

&lt;223&gt; complement component 4a (C4A) gene.

&lt;400&gt; 413

```
agaaggtagc agacagacag acggatctaa cctctcttgg atcctccagc catgaggctg 60
ctctgggggc tgatctgggc atccagcttc ttcaccttat ctctgcagaa gccaggttg 120
ctcttggttct ctcttctgtt ggttcatctg ggg gtcccc tatcgggtggg ggtgcagctc 180
caggatgtgc cccgaggaca ggtagtgaag ggatcagtggt tcttgagaaa cccatctcgt 240
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ctcctcagtc tccaggtgac cttgaaagat gcgaagagct gtggcctcca tcaactcctc 360
agaggccctg aggtccagct ggtggcccat tgcctatggc taaaggactc tctgtccaga 420
acgacaaaca tccagggtat caacctgctc ttctcctctc gccgggggca cctctttttg 480
cagacggacc agcccattta caacctggc cagcgggttc ggtaccgggt ctttgctctg 540
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ctccgcgtgc ggaagaagga ggtgtacatg ccctcgtcca tcttccagga tgactttgtg 660
atcccagaca tctcagagcc agggacctgg aagatctcag cccgattctc agatggcctg 720
gaatccaaca gcagcaccga gtttgaggtg aagaaatatg tcttcccaa ctttgaggtg 780
aagatcacc ctggaaagcc ctacatctg a cggtgccag gccatcttga tgaaatgcag 840
ttagacatcc aggcaggta catctatggg aagccagtgc agggggtggc atatgtgctg 900
tttgggctcc tagatgagga tggtaagaag actttcttcc gggggttga gagtcagacc 960
aagctggtga atggacagag ccacatttcc ctctcaaagg cagagttcca ggaagccctg 1020
gagaagctga atatgggcat tactgacctc caggggctgc gcctctacgt tgctgcagcc 1080
atcattgagt ctccaggtgg ggagatggag gaggcagagc tcacatctg gtattttgtg 1140
tcctctccct tctccttggg tcttagcaag accaagcgac accttggtgc tggggccccc 1200
ttctgtctgc aggccttggg ccgtgagatg tcaggctccc cagcttct gg cattcctgtc 1260
aaagtttctg ccacgggtgtc ttctcctggg tctgttctg aagcccagga cattcagcaa 1320
aacacagacg ggagcggcca agtcagcatt ccaataatta tccctcagac catctcagag 1380
ctgcagctct cagtatctgc aggtctccca ctccagcga tagccaggct cactgtggca 1440
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cgtgttgggg acactctgaa cctgaacttg cgagccgtgg gcagtggggc caccttttct 1560
cattactact acatgacct atcccagggg cagatcgtgt tcatgaatcg agagcccaag 1620
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gtggccttct actaccatgg agaccacca gtggccaact ccctgcgagt ggatgtccag 1740
gctggggcct gcgagggcaa gctggagctc agcgtggacg gtgccaagca gtaccggaac 1800
```

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ggggagtcg tgaagctcca ottagaaacc gactccctag ccctggtggc gctgggagcc 1860  
 ttggacacag ctctgtatgc tgcaggcagc aagtcc caca agccccctcaa catgggcaag 1920  
 gtctttgaag ctatgaacag ctatgacctc ggctgtggtc ctgggggtgg ggacagtgcc 1980  
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 caaaaggcga ttaatgagaa attgggtcag tatgcttccc cgacagccaa gcgctgctgc 2160  
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 aagaagagca gggacaagg ccaggcgggc ctccaacgag ccctggagat cctgcaggag 2340  
 gaggacctga ttgatgagga tgacattccc gtgcgcagct tcttcccaga gaactggctc 2400  
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 gatccattgg acactttagg ccttgagggt gccttctcac caggaggcgt ggccctccctc 3060  
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 gcttcccgtc acctggacaa gacagagcag tggagcacac tgcctcccga gaccaaggac 3180  
 cagcccgctg atctgatcca gaaaggctac atgcggatcc agcagtttcg gaaggcggat 3240  
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 tctaactggc ttctgtccca gcagcaggct gacggtctgt tccaggacc c tgtccagtg 3420  
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 tttgtgacca tgccttca tcatgggctg gccgtcttc aggatgaggg tgcagagcca 3540  
 ttgaagcaga gagtggaaag ctccatctca aaggcaact catttttggg ggagaaagca 3600  
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 aaggcgccctg tggacctgct cgggtgttgc cacaacaacc tcatggcaat ggcccaggag 3720  
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 accccggctc ctgcgaaccc atccgacccc atgccccagg cccagccct gtggattgaa 3840  
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 gacacggtga ttgccctgga tgccctgtct gcctactgga ttgcctcca caccactgag 4020  
 gagaggggtc tcaatgtgac tctcagctcc acaggccgga atgggttcaa gtcccacgcg 4080  
 ctgcagctga acaaccgcca gattcgcggc ctggaggagg agctgcagtt ttccttgggc 4140  
 agcaagatca atgtgaaggt gggaggaac agcaaggaa ccctgaaggt ccttcgtacc 4200  
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<210> 414  
<211> 408  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(408)  
<223> 3' terminal sequence. cd3g antigen, gamma  
polypeptide (tit3 complex) (CD3G) gene.

<400> 414  
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<210> 415  
<211> 457  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(457)  
<223> 5' terminal sequence. cd3g antigen, gamma  
polypeptide (tit3 complex) (CD3G) gene.

<400> 415  
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gcagaagcca aaaatatcac atggtttaaa gatgggaaga tgatcggtt cctaactgaa 120  
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aagatgacca gtacagccac cttcaagggn aaccagt 457

<210> 416  
<211> 822  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature

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&lt;222&gt; (1)..(822)

&lt;223&gt; cd3g antigen, gamma polypeptide (tit3 complex) (CD3G) gene.

&lt;400&gt; 416

```
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&lt;210&gt; 417

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(439)

<223> 3' terminal sequence. v-rel avian  
reticuloendotheliosis viral oncogene homolog b  
(nuclear factor of kappa light polypeptide gene  
enhancer in b-cells 3) (RELB) gene.

&lt;400&gt; 417

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gccgccccca aaggccgct 43 9
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&lt;210&gt; 418

&lt;211&gt; 234

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(234)

<223> 5' terminal sequence. v-rel avian  
reticuloendotheliosis viral oncogene homolog b

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(nuclear factor of kappa light polypeptide gene  
enhancer in b-cells 3) (RELB) gene.

&lt;400&gt; 418

```
acgggggatg cccaacgtcc ttggggagct gaacagtctg gaccccatg gcatcgagag 60
caaacggcgg aagaaaaagc cggccatcct ggaccacttc ctgcccaccc acggctcagg 120
cccgttcctc ccgcccgcag cctgctgcc agaccctgac ttcttctctg ggcaccgtgt 180
tccttgcccg gcngggaggc cctggggggc ctgnacctcc tgggacgatg ggtt      234
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&lt;210&gt; 419

&lt;211&gt; 2314

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2314)

<223> v-rel avian reticuloendotheliosis viral  
oncogene homolog b (nuclear factor of kappa light  
polypeptide gene enhancer in b -cells 3) (RELB)  
gene.

&lt;400&gt; 419

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&lt;210&gt; 420

&lt;211&gt; 214

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(214)

<223> 3' terminal sequence. estrogen receptor 1  
(ESR1) gene.

&lt;400&gt; 420

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gagcatcccg ctggattctt ttcaaagtg caaaagaggt ttacaagtgt gtttcattaa 120  
acaaagcaaa gctgcgacaa aaccgagtca catcagtaat agtatgcatc ggcaaaaggg 180  
catattaatc catcaaacac aatttggcat ttga 214

&lt;210&gt; 421

&lt;211&gt; 520

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(520)

<223> 5' terminal sequence. estrogen receptor 1  
(ESR1) gene.

&lt;400&gt; 421

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cagtgtagag ctcttgtttt atgggaaaag gctcaaatgc 520

&lt;210&gt; 422

&lt;211&gt; 6450

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(6450)  
<223> estrogen receptor 1 (ESR1) gene.

<400> 422  
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gaagaaagaa caacatcagc agtaaagtcc atggaatagc tagtggtctg tgtttctttt 5160
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gtgcagctct tgatttgatt tccctagtaa ccttgagat atgtttaacc aagccatagc 5340
ccatgccttt tgagggtcga acaataagg gacttactga taatttactt ttgatcacat 5400
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ctttccaatt gaattaaagt gtggcctcgt ttttagtcat ttaaaattgt tttctaagta 5880
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gttccaaac catcgtcagt gtgtgtgttt agagctgtgc accctagaaa caacatactt 6060
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caatgctttt tgtgactac atactcttca gtgtagagct cttgttttat gggaaaaggc 6240
tcaaatgcca aattgtgttt gatggattaa tatgcccttt tgccgatgca tactattact 6300
gatgtgactc ggttttgtcg cagctttgct ttgtttaatg aaacacactt gtaaacctct 6360
tttgactttt gaaaaagaat ccagcgggat gctcgagcac ctgtaaacaa ttttctcaac 6420
ctatttgatg ttcaataaaa gaattaaact 6450

```

&lt;210&gt; 423

&lt;211&gt; 580

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(580)

&lt;223&gt; 3' terminal sequence. pre -b-cell leukemia transcription factor 1 (PBX1) gene.

&lt;400&gt; 423

```
ttaaactgtac aaacactttt attattttct ttgtaatttt tttcctcttt aaattcctct 60
aattgttgaa aatatccttc agtgatatgc gagagggcgg gcacccggga gtctaggaca 120
gaggcacagg ggcagggaag atgacgaaaa ccaggctgac agctggaggc agggaagggt 180
ggcttctacc cagaaaaaaa aggggagaga gtataaagaa gtgtccagat tggctgaaat 240
agcatcccaa agaagagaag agaaggagac tottattgtg ttgc tgatt gcttogacct 300
ccagtctgac cgcttcaggn ttgggagaga aaccctccct tcctgcccct gcccactg 360
ggcgacaggg tcagccggga tgcgattgct gggagatcag ttggaggtat cagagtgaac 420
actgccaggg ccttctgtag gggaggtcac tgatgaagg gtagtagcat cctgccaacc 480
tccattagca ctgatgcct gcg gactgta catctgactg gctgcgagtc catcactgta 540
tcctcctgtc tggctgataa catggcgaag ggtatccacc 580
```

&lt;210&gt; 424

&lt;211&gt; 503

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(503)

&lt;223&gt; 5' terminal sequence. pre -b-cell leukemia transcription factor 1 (PBX1) gene.

&lt;400&gt; 424

```
gccaaagagg agttagccaa gaagtgtggc accacagtct cccaggatc acaactggtt 60
tggaaataag cgaatccggt acaagaagaa cataggtaaa tttcaagagg aagccaatat 120
ttatgtctgc aaaacagctg tctactgtac caatgtgtca gcccatggaa gccaagctaa 180
ctcgccctca actcccaact cggctggtgg atacccttcg ccatgttatc agccagacag 240
gaggatacag tgatggactc gcagccagtc agatgtacag tccgcaggca tcagtgtctaa 300
tggagggttg caggatgcta ctacccttc atcagtgacc t cccctacag aaggccctgg 360
cagtgttcac tctgatacct ccaactgata tcccagcaat cgcaccccg ctgaccctgt 420
gccccagttg ggcaggggca ggaggagggt tttctctccc aacgctgaag cggtcagact 480
ggagggtcaaa cgattaggca aac 503
```

&lt;210&gt; 425

&lt;211&gt; 1819

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1819)

&lt;223&gt; pre-b-cell leukemia transcription factor 1 (PBX1) gene.

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&lt;400&gt; 425

```

cttccctgtt tatcctgaaa aggatttgaa g acaagcttg aaggataaaa agccttggtg 60
cttcccagga gccgagccga ggagcagaag aggaagagcc gggggtgcc gtagcctttg 120
gagatggacg agcagcccag gctgatgcat tcccatgctg gggtcgggat ggccggacac 180
cccggcctgt cccagcactt gcaggatggg gccggaggga ccgaggggga gggcgggagg 240
aagcaggaca ttggagacat tttacagcaa attatgacca tcacagacca gagtttggat 300
gaggcgcagg ccagaaaaca tgctttaaac tgccacagaa tgaagcctgc cttgtttaat 360
gtgttggtg aaatcaaaga aaaaacagtt ttgagtatcc gaggagccca ggaggaggaa 420
cccacagacc cccagctgat gcgctggac aacatgctgt tagcggaagg cg tggcgggg 480
cctgagaagg gcgaggggtc gcggcagcg gcggcagcg cgcgcgcttc tggaggggca 540
ggttcagaca actcagtga gcattcagat tacagagcca aactctcaca gatcagacaa 600
atctaccata cggagctgga gaaatacag caggcctgca acgagttcac caccacgtg 660
atgaatctcc tgcgagaca aagccggacc aggccatct ccccaaagga gattgagcgg 720
atggtcagca tcatccaccg caagttcagc tccatccaga tgcagctcaa gcagagcacg 780
tgcgaggcgg tgatgatcct gcgttcccga tttctggatg cgcgcgga gagacggaat 840
ttcaacaagc aagcgacaga aatcctgaat gaatatttct attcccatct cagcaaccct 900
taccacagtg aggaagccaa agaggagtta gccaaagaat gtggcatcac agtctcccag 960
gtatcaaact ggtttgaaa taagcgaatc cgttacaaga agaacatagg taaatttcaa 1020
gaggaagcca atatttatg tgccaaaaca gctgtcactg ctaccaatgt gtcagcccat 1080
ggaagccaa ctaactcgcc ctcaactccc aactcggctg gttcttcca g ttttttaac 1140
atgtcaaact ctggagattt gttcatgagc gtgcagtcac tcaatgggga ttcttaccaa 1200
ggggcccagg ttggagccaa cgtgcaatca cagggtggata cccttcgcca tgttatcagc 1260
cagacaggag gatacagtga tggactcgca gccagtcaga tgtacagtcc gcagggcatc 1320
agtgttaatg gaggttggca gga tgctact acccctcat cagtgaacct ccctacagaa 1380
ggccctggca gtgttcaact tgatacctcc aactgatctc ccagcaatcg catcccggct 1440
gaccctctgc cccagtggg gcaggggcag gagggagggt ttctctccca agctgaagcg 1500
gtcagactgg aggtcgaagc aatcagcaaa cacaataaga gtctccttct cttctcttct 15 60
ttgggatgct atttcagcca atctggacac ttctttatac tctcttccct ttttttctg 1620
ggtagaagcc acccttccct gcctccagct gtcagcctgg tttctgcat cttccctgcc 1680
cctgtgcctc tgtcctagac ttcccggggg ccccgccctc tctcatatca ctgaaggata 1740
ttttcaacaa ttagaggaat ttaaagagga aaaaaat tac aaagaaaata ataaaagtg 1800
ttgtacgttt tcaaaaaaa 1819

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&lt;210&gt; 426

&lt;211&gt; 506

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(506)

&lt;223&gt; 3' terminal sequence. gli -kruppel family

member gli3 (greig cephalopolysyndactyly syndrome)

(GLI3) gene.

&lt;400&gt; 426

```

taaaaagagg gtggtttgag tgtaacaata ctgattcaaa actgaaatgg aagacagttt 60
ctccctagaa tacttttagg tttttcagag tccttttcca taaa aggaat ataattgaaa 120
cacatctcag ttaggtgaga tgagattgct aaaatacata cagaactaaa aaaacagcca 180
aaacaaagtc agttttaatct cttcaactcc taatgatttc cggttggttc agtctttttt 240
tcctaaagcc tattgcataa ctgcaaggga attgctttct tccgctaggg aggtcagcaa 300
agaactcatg tccccgatag cc atgttggt ggtgctcatg gacagcgctg ggaatgggag 360
ggacgcccga gggctggtta aagccggaag aaactatgga aaaggtctca atgatacttg 420
ggctcagggc cccgacatca ggctcgagtg gtcccatct ctatgattgc atcgaagtca 480
atctggtacc ctcccaggcc aggctg 506

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<210> 427  
<211> 239  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(239)  
<223> 5' terminal sequence. gli -kruppel family  
member gli3 (greig cephalopolysyndactyly syndr ome)  
(GLI3) gene.

<400> 427  
ggcagaagga tcacttgagg ccaggcattc aagaccagcc tatgcaagat aatgagacct 60  
tgtctctatt taaaaaacia aaagcctggt gtggtggtgc atgcctgtag tctcagcctc 120  
ctgagtagct gggactataa gcacgcacca ctatgtctgg ctaatttttg tatttttagt 180  
agagacaggg ttccaccacg ttgcccaggg cagtcttgaa ctctgaccc caagtgatc 239

<210> 428  
<211> 5054  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(5054)  
<223> gli-kruppel family member gl i3 (greig  
cephalopolysyndactyly syndrome) (GLI3) gene.

<400> 428  
cgatactacg tgggcatttt tggtcgaaga gagctgaagt aatgagaaga catcatggag 60  
gccagtgccc acagctccac gaccactgaa aagaaaaaag ttgagaattc catagtgaag 120  
tgctccactc gaacagatgt gagcgagaaa gccgttgccct ccagcaccac ttctaagtag 180  
gatgaaagtc ctggacagac ttatcacaga gagagaagaa acgcaatcac tatgcagcca 240  
cagaatgtcc aggggctcag caaagtcagt gaggaacctt caacatcgag tgacgagagg 300  
gcctcattga tcaagaaaga gatccatggg tccctgccac acgtggcgga gccctctgtg 360  
ccgtaccgag ggacggtgtt tgccatggac cccaggaatg gttacatgga gcccactac 420  
caccctcctc atcttttccc tgccttccat cctcctgtac caattgatgc cagacatcat 480  
gagggcggtt accattacga tccatctccg attcctc

cat tgcatatgac ttccgcctta 540  
tctagtagcc ctacgtatcc ggacctgccc ttcattagga tctcccaca ccggaacc cc 600  
gctgctgctt ccgagtctcc cttcagccct ccacatccct acattaatcc ctacatggac 660  
tatatccgct cttgcacag cagcccatcg ctctccatga tctcagcaac ccgtgggctg 720  
agccctacag atgcgcccc tgaggagtc agcccagcag aatactatca tcagatggcc 780  
ctgctaactg gccagcgag cccctatgca gacatt attc cctcagctgc caccgcccgc 840  
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agccctgctt tgagcttcac ctactcttcc gcgcccgtct ctctccacat gcatcagcag 1140  
atcctaagcc gacaacagag cttaggttca gcctttggac acagccctcc actcatccac 1200  
cctgccccaa cttttccaac acagaggcct attccaggga tccctacggt tc tgaacccc 1260

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gtccagggtca gctccggccc ttctgagtc tccacagaaca agcccacgag tgagtctgca 1320  
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 ctccccagcc caggggctcg ggggcagcag gaacagcccg aaggaacaac ccttgtcaag 1440  
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 aaccccttga ggcagggggtg tgctgggggc tatcagaccc tcggggagaa cagcaacccc 3720  
 tacggtggcc cagagcactt gatgctccac aacagccccg gaagtggcac cagtggaaac 3780  
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 cagatgcttg ggcagattag tgctacctca cacatcaaca tctaccaagg gccagagagc 4140  
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 ttctatgac aaaccgtggg ctctcagtcag caagacaga aagctggttc attctctatt 4440  
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 cagattgact tcgatgccat catagacgat ggggaccact ccagcctgat gtcggggggc 4620  
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 ttaggaaaaa aagactgcaa ccaacggaaa tcaataggag ttgaagagat taaactgact 4860  
 ttgttttggc tgttttttta gttctgtatg tatttttagca atctcatctc accttaactga 4920

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gatgtgtttc aattatattc tttttatgga aaaggactct gaaaaaccct aaagtattct 4980  
aggagagaaac tgtcttccat ttcagttttg aatcagtatt gttacactca aaccaccctc 5040  
tttttaaaaa aaaa 5054

<210> 429  
<211> 271  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(271)  
<223> 3' terminal sequence. interleukin enhancer  
binding factor 1 (ILF1) gene.

<400> 429  
aggagacttg ttttactcag agtggaaaat ttgccaggg acaaagtc aa cacaaagaaa 60  
caaacaacaa aaaatagcca gaaagagaac agttaagtgc agtcggtga gtcccggcag 120  
ttccttcccg gcaactggctc gtccctgggt tctcaagggt ccatgcggcc acagcgtccg 180  
tccacctgtc cacgcgagcc acatgctgaa atggagggtg ataaaattca tcaggcagct 240  
gctgtaacac ggaaatgtgc agatgcc aga g 271

<210> 430  
<211> 193  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(193)  
<223> 5' terminal sequence. Similar to Retinoblastoma -like protein 2,  
sw|Q08999|RBL2\_HUMAN.

<400> 430  
TGTCTACATT TNCCCACATA AAAATGAAAC AATNNTTCT CCTCGNGAAA AGATTTTATA 60  
TTACTTNAGC NAAAGTCCTT CAAAGNGACT GAGCGNANNT AATAGTNTGA TACGCATAGG 120  
NGNAACTCCT ACTNNAANGN GCGGNNTTCT TNTNGNGAT GGCNGTGAAT NCACTGCAAA 180  
NAGCATTTGC CCN 193

<210> 431  
<211> 184  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(184)  
<223> 3' terminal sequence. Homo sapiens CD2 antigen (p50).



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<400> 431  
AGTCAAAGCT TTTATTTCAC TTTNACTCAC AGGATGGGGG GCAAGTNTCC ACCAGGGCAC 60  
ATAAGAAACT CCAGAGTCTC TTAAGCAGAT AGGCTGCTTG TAGNGAGACC CAGGNACACC 120  
AATCAGTTGA TTTATCGCAT CTACACATGA CCNGAGAGGG GACAAGAAAT CTCTAAGTTT 180  
TCTG 184

<210> 432  
<211> 242  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(242)  
<223> 5' terminal sequence. Similar t o NM\_022641 Homo sapiens  
chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1)

<400> 432  
ATTCGGCACG ATGACTGGCC AGGGTATAAA AAGGGCCAC AAGAGACCGG CTCTAGGATC 60  
CCAAGGCCCA ACTCCCGAA CCACTCAGGG TCCTGTGGCA GCTCACCTAG TGGCAATGGC 120  
TCCAGGCTCC CGGAACGTCC CTGATCCTGG NTTTGNCT NCTCTNACTG CCCTGGNTTN 180  
AANAAGCTNG TGCCNTCCAA ANCGTCCGT TATCCAGGGT TTTTGACCAC GCTATGCTNC 240  
AA 242

<210> 433  
<211> 329  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(329)  
<223> 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 433  
AACAGTCACC GACAACATGC TGTGTGCTGG AGACACTCGG AGCGGCGGGC CCCAGGNAAA 60  
CTTGACGAC GCCTGCCAGG GNATTTCGGG AGGCCCCCTG GTGTGTCTGA ACGATGGCCG 120  
CATGACTTTG GTGGGCATCA TCAGCTGGGG CCTGGGCTNT GGACAGAAGG ATGTCCCGGG 180  
TGTGTACACC AAGGTTACCA ACTACCTAGA CTGGATTCGT GACAACATGC GACCGTGACC 240  
AGGAACACCC GACTCCTCAA AAGNAAATGA GATCCCGNCT CTTCTTCTTC AG AAGACACT 300  
GCAAAGGCGC AGTGCTTCTC TACAGACTT 329

<210> 434  
<211> 247  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature

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&lt;222&gt; (1)..(247)

&lt;223&gt; 3' terminal sequence. Homo sapiens plasminogen activator (PLAT)

&lt;400&gt; 434

```
AAATATATCT GAANNNTTA AGTACAGTNT AAAACAGGGT TNTGGCAACA GAAAGTAAAA 60
ACTAACATGG NTGCTATAA ATATGCTGAA GCCTAGTTGT TCAAATGATA CAATTCTCTC 120
ATGCTACTCT AAAGTTTNTA AAGNAAAAGG GTTTACACTT TACACACT GT ACACAAAGGG 180
GNTACCTTCT GNGNGCCNGG GAGTGGGGAA AGGGGANGGN GACTTGACGT CAAGGGTGCT 240
TTTGAGG                                         247
```

&lt;210&gt; 435

&lt;211&gt; 63

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(63)

&lt;223&gt; 5' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

&lt;400&gt; 435

```
CCGCCAGNAC CTGCGTATCC GCACTGTTCA GCCAAGCCT GACTATGGAG CTGCTGTGGC 60
TTT                                         63
```

&lt;210&gt; 436

&lt;211&gt; 190

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(190)

&lt;223&gt; 3' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

&lt;400&gt; 436

```
GAAGAGGAGG NCCTTGGCAC TGGTNGGGAN GGAAGCCCCA GGGGAAAAGG TTNAGGAGTC 60
CCAGGGCTCA GCTGTCACTG GGCAGGGCAG GCACACTGGC AGGGCCAGGC AGCAGGCNNG 120
TATATATGNC CACCCACGG AGGAACACAG CCTNATGCAG NCGTTNATCG TGGTNGTGCA 180
GNAGCACAGG                                         190
```

&lt;210&gt; 437

&lt;211&gt; 176

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(176)

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<223> 3' terminal sequence. Homo sapiens E74 -like factor 1 (ets domain transcription factor) (ELF1)

<400> 437

CCCTTAGGCT GTTCTGGTGA TGAGGCTCCC GGTGAGTCTG CATATTTTNN TTGCACCTGC 60  
TGTGTTTCCA TCACTTCAGG AATCCCATCT AATGTGACGG ACACATGGGT GACTGGGGCA 120  
ACAACCATGT CATCTTCAGG NGAACATAAT ATATTATTAT TTATCCGGTT TTCATC 176

<210> 438

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(465)

<223> 5' terminal sequence. Homo sapiens selectin P,  
granule membrane protein CD62, SELP

<400> 438

NGGAACATAT GGAGTTTTTA CA AACGCTGC ATTTGACCCG AGTCCTTAAG AGACCTGTCC 60  
TTTTCTGGT CTCCTCATTC AGCCTCCATA TGATCCTGTT GTGAACATCA AGTTTCCTGC 120  
TACACTGGAC TTAACATATAA TGCAATTTGCT GCAGGTTTCC ATAAACACCC ATGANTCAAA 180  
GACATGGAAT TACCTTAGAT TAGCTCTGGA CCAGCCTGTT GGACCCGCTC TGGACCAACC 240  
CTGTTTCCTG AGTTTGGGAT TGTGGTACAA TCTCAAATTC TCAACCTACC ACCCCTTCCT 300  
GTCCACCTC TTCTCTTCTT GTAACACAAG CCACAGAAGC CAGGAGCAAA TGTTCCTGCA 360  
GTAGTCTCTG TGCTTTGACT CACCTGTTAC TTGAAATACC AGTGAACCAA AGAGACTGGA 420  
GCATCTGGAC TTNACAAGAA GACCAGACTT GTGGAGANAT TAA AA 465

<210> 439

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(396)

<223> 3' terminal sequence. Homo sapiens selectin P,  
granule membrane protein CD62, SELP

<400> 439

GAAAATCCTT TNAATTACGN ATTTNAANAT TGGNCTTTGG GNCATTTGAG GGACAGTGAC 60  
TGGGGGCAGG AAGGCCACAG GNGACATGTG GCCTTCTAGC TTATNCTTG GCCTTCTGCA 120  
GCCTCTGGGG CCATCCAGAG GACTCTCTGG AAGCCTCAGA GCAGAGGNCC AAGAGGCCTC 180  
ATCAACAGCA ACCANTGGAG ACTCCAGAAG ATGCTACAGG ANTTNCTCCC AATTAGAGAT 240  
GCCACCTGTT TNCCAACAAA GTGGAGAAAA CCTTCCTNNA ATCAAAAANT AAAGAGGTNT 300  
TTCNATTTCT CCACAGTTTG GCCTCCTTGT GAGTCAGATG NTCCAGTCTC TTTGGNNCAC 360  
TGGTATTCA AGTAACAGGT GAGNNAAAGG ANAGAG 39 6

<210> 440

<211> 337

<212> DNA

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(337)

&lt;223&gt; 5' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

&lt;400&gt; 440

```
AAAGGCTCAG CAGTTGAC CT GGGACCTTAA CAGAAATGTG ACCGATATCG AGTGTGTTAA 60
AGACGCCGAC TATTCTATGC CGGCAGTGAA CAATAGCTAT TGCCAGTTTG GAGCAATTTC 120
CTTATGTGAA GTGACCAACT ACACCGTCCG AGTGGCCAAC CCCCATTCT CCACGTGGAT 180
CCTCTTCCTT GAGAACAGTG GGAAGCCTTT GGCAGGTGCG GAGAATCTGA CCTGCTNGAT 240
TCATGACGTT GATTCTCTGA GCTGCAGCTG GCGGGTAGGG CCGGGGCCCC CGCGGGACGT 300
CCAGTACGAC CTGTACTTGA ACGTTNCCAA CAGGNGT 337
```

&lt;210&gt; 441

&lt;211&gt; 104

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:prim er

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(104)

&lt;223&gt; 3' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

&lt;400&gt; 441

```
TTCCCCGCTC CCAGACCACC AGNTTGNCGT TTTGGNAGNT NTNACCGANG GGGTNTTNCA 60
TGTNAGGGNT NCGGNAAAN AGTTNTGAA NCACCAGAAA CCTT 104
```

&lt;210&gt; 442

&lt;211&gt; 223

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(223)

&lt;223&gt; 5' terminal sequence. Human tumor protein p53 (Li -Fraumeni syndrome) (TP53)

&lt;400&gt; 442

```
AAGCAATGGA TGATTGATG CTGTCCCCGG ACGATATTGA ACAATGGTTC ACTGAAGACC 60
CAGGTCCAGA TGAAGCTCCC AGAATGCCAG AGNTGNCTCC CCGCGTGGCC CCTGCACCAG 120
CAGCTCCTAC ACCGCGNGCC CCTGCACCAG CCCCCTCCTG GCCCTGTCA TCTTCTGTCC 180
CTTCCAGAN AACCTACCAG GGCAGCTACG GTTTCGGTCT G GG 223
```

&lt;210&gt; 443

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<211> 223  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(223)  
<223> 5' terminal sequence. Tumor protein p53  
(Li-Fraumeni syndrome) (TP53) gene.

<400> 443  
aagcaatgga tgatttgatg ctgtccccgg acgatattga acaatgggtc actgaagacc 60  
caggtccaga tgaagctccc agaatgccag agntgnctcc ccgcgtggcc cctgcaccag 120  
cagctcctac accggcngcc cctgcaccag cccctcctg gccctgtca tcttctgtcc 180  
cttcccgan aacctaccag ggcagctaag gtttccgtct ggg

<210> 444  
<211> 343  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(343)  
<223> 3' terminal sequence.

<220>  
<221> misc\_feature  
<222> (1)..(343)  
<223> v-erb-b2 avian erythroblastic leukemia viral  
oncogene homolog 2 (neuro/glioblastoma derived  
oncogene homolog) (ERBB2) gene.

<400> 444  
caaggggctg caaactnncc cacacatgac ccagccctc tacagcggta cagtgaggac 60  
cccacagtac ccctgcctc tgagactgat ggctacgttg cccccctgac ctgcagcccc 120  
cagcctgaat atgtgaacca gccagatgtt cggccccagc ccccttcgcc ccgagaggcc 180  
ctctgcctgc tgcccgaact gctggtgcc ctctggaaag gcccaagact ctctccccag 240  
ggaagaatgg ggtcgtcaaa gagtttttgc cttt gggggt gccgtgggag aacccccgagt 300  
attgacaccc caggggaggg agcttgccct tcagccccac ctt 343

<210> 445  
<211> 309  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(309)  
<223> 3' terminal séquence.

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<220>  
<221> misc\_feature  
<222> (1)..(309)  
<223> zinc finger protein 144 (Mel -18) (ZNF144) gene.

<400> 445  
ccgcccccca cccccaaggt gganagagct ggggaaagta gaagagggtg aaaaaagggc 60  
ccagaaaaag tggaaggagt ggagaggctt ag ctggaaga agggagaggg tccctggcct 120  
caagttaagg ggggcacggg agcgccnttg acagtcattt tgcgccccct gctggtnгаа 180  
ganggtttct tcaggcagtt caagctaccc ccgttngcan ctttngnngc cccacttgct 240  
ntcgaagggg ganttgggna ngtagggtnг gtngcttgan gcccatngga actnggaaaa 300  
ccatnggat 309

<210> 446  
<211> 268  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(268)  
<223> 3' terminal sequence.

<220>  
<221> misc\_feature  
<222> (1)..(268)  
<223> MAP/microtubule affinity-regulating kinase 3  
(MARK3) gene.

<400> 446  
attatcttgt gaatctactt agaaaaacac acacaagcaa tggtcacaac tataaattta 60  
aaccttttgc actaaaaaaa cacaaaacaa caaacacaan accacaggca tgaactgtaa 120  
acctgtatta actntgaact ggtcttaagg ttaattctta gcngtcattc agtattttcc 180  
tccttgcaa ctgtaatgtt ttngcaccgg ntgatctccc gcngggggta ctagtaatga 240  
ctggctgccc gtgtagggag atgcttcc 268

<210> 447  
<211> 169  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(169)  
<223> 5' terminal sequence.

<220>  
<221> misc\_feature  
<222> (1)..(169)  
<223> MAP/microtubule affinity-regulating kinase 3  
(MARK3) gene.

<400> 447

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gaacactgat ggaaatgtat agaataatat ttaggcaata acgtctgcat cttctaaatc 60  
atgaaattaa agtctgagga cgagagcacg nctgggngcg aaantntgcc tttttntac 120  
ggatgcacta cantaaagan gtgcanccta tncgcccct gccctactt 169

&lt;210&gt; 448

&lt;211&gt; 393

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(393)

&lt;223&gt; 3' terminal sequence.

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(393)

&lt;223&gt; EST N68536 MAX-interacting protein 1 (MXI1) gene.

&lt;400&gt; 448

aagtaattaa gggtagttaa attattttaa gtatacaaag tccaaacagc caggggtaag 60  
gtctccaaga ggccttccca gggttaaggga gagggccaca agggaacctt ggagtttgaa 120  
agacaaaggg aacacatgac atcaaagtgc aggctagaaa tttcacttag aagaaaataa 1 80  
cattactgaa aatattcgta agagtaacaa tagcacatgc acagtgggac tgtgaggaag 240  
agagagactg cctgtaggaa aatggaagca aatctttaca ttaaaatgag acaagtgctg 300  
aacttactat gttaactatg atagtgtgtc tacnatagat atcncgatgg ttaaaagctg 360  
gtaaaaggta atggttctca aaaccnaaa a tag 393

&lt;210&gt; 449

&lt;211&gt; 217

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(217)

&lt;223&gt; 5' terminal sequence.

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(217)

&lt;223&gt; EST R81126 lymphotoxin beta receptor (LTBR) gene.

&lt;400&gt; 449

ttacctgggt atctcctact gtagtatgag gaagaatggc tgtaaatgta ttttttgaat 60  
tctggnctca cctttgtctc agctaaatgt agccgcatcc gggacacagt ttgtgccaca 120  
tgtgccgaga attcctacaa cgagc actgg aactacctga ccattctgcca nctgtgccgc 180  
ccctgtgacc cagtgatggg cctcgnctga gantgcc 217

&lt;210&gt; 450

&lt;211&gt; 157

&lt;212&gt; ADN

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(157)

&lt;223&gt; 5' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(157)

&lt;223&gt; (POU2F2) gene.

&lt;400&gt; 450

```
nattcggcaa cgnggaaagg aaagaaacta accaacaaaa gagaaaacca aaaataatca 60
caacagaaac cagctgcccc aaaggaggcc agtngtnggg acgcagaggg tcc tcagagc 120
aggagtnaca agggaggaaa gaccaaaaaa acaacca                               157
```

&lt;210&gt; 451

&lt;211&gt; 282

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(282)

&lt;223&gt; 5' terminal sequence.

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(282)

<223> caspase 4, apoptosis -related cysteine protease  
(CASP4) (ex CASP1)

&lt;400&gt; 451

```
gagaatctga cagccaggga tatggagtca gcgctgaggg catttgctac cagaccagag 60
cacaagtccct ctgacagcac attcttggtta ctcattgtctc atggcatcct ggagggaatc 120
tgcggaactg tgcatgatga gaaaaaacca gatgtgctgc tttatgacac catcttccag 180
atattcaaca accgcaactt gcctcagtct ngaaggacaa acccaaggtc atcattgtnc 240
agggcttgca gagggtgcaa accttggggg aantttgggg tc                               282
```

&lt;210&gt; 452

&lt;211&gt; 424

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(424)

&lt;223&gt; 5' terminal sequence



<220>  
<221> misc\_feature  
<222> (1)..(424)  
<223> syndecan 1 (SDC1) (ex HRB)

<400> 452  
ttgcttttng caaaactcta cttaatccaa tnggtttttc cctgtacagt agattttcca 60  
aatgtaataa actttaatat aaagtagtcc tgtgaatgcc actgccttcg cttcttgcc 120  
ctgtgctgtg tgtgacgtga cgggactttt ctgcaaacac caacatgttg ggaaacttgg 180  
ctcgaatctc tgtgccttcg tctttcccat ggggagggga ttctgggtcc agggccctc 240  
tgtgtatttg cttttttgtt ttggctgaaa ttctcctgga ngtcggtagg ttcagccaag 300  
gttttataag ggctgatgtc aatttntctgt gtttgccaan ttccaagccc catcttncta 360  
aatgggcaaa aggaaggttg gatgggcccc agcnacagct ttgnacc ga gggctnttgg 420  
gtca 424

<210> 453  
<211> 435  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(435)  
<223> 5' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(435)  
<223> Integrin, beta 2 (antigen CD18 (p95), lymphocyte  
function-associated antigen 1; macrophage antigen  
1 (mac-1) beta subunit) (ITGB2)

<400> 453  
aggagtcccc cggctgcccc tcacct gtg gcaagtacat ctctgcgcc gagtgccctga 60  
agttcgaataa gggccctnt ggaagaactg cagcgcgccg tgtccgggcc tgcagctgtc 120  
gaacaacccc gtgaaggcca ggacctgcaa ggagaggac tcagagggt gctgggtggc 180  
ctacacgctg gagcagcagg acgggatgga ccgctacctc atctatgttg atgagagccg 240  
agagtgtgtg gcaggcccca acatgcgcgc catcgtcggg ggcaccgttg gcaggcatcg 300  
tgctgatcgg cattctctctg ctggtcatct gggaaggctc tgatccacct gagcgacctc 360  
cgggagttac agcggttttg agnaggagaa gctcaagtcc cagtnggaac aatgattatt 420  
ccctttttca agagc 435

<210> 454  
<211> 544  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(544)

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&lt;223&gt; 5' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(544)

&lt;223&gt; Protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)

&lt;400&gt; 454

```
gtgtgaccag acatgcaacc gncatctatg gtttctacgn atgnagtgnc aagcagnacg 60
nctnacaaca tcaaactgtg gnaaaacctt cactgnactg ncttcaactg ncctgnccca 1 20
tcgcggncca tagtggacgt aaaagatctt ctgncctgncc acggaggcct gttccccgga 180
cctgncagtt ctatggnagc agattcggcg ggatcatgcg gccacacagat gtgtcctgta 240
ccaggggcct gctgtgtgac ctgctgtggt ctgaccctga caaggacgtg cagggtctggg 300
gcgagaaacga ccgtgggcgt ctcttttac c tttggagccg aggtggtggc caagttcctc 360
cacaagcacg acttgacact catctgccga gcacaccagg ttgtagaaga cggctacgag 420
ttctttgccg agcggcantt ggtgacactt ttctcagctt ccaactactg ttgcgagttt 480
nacaatgctt gcgccatgat gagtgtgacg agaccctatg tgcttttcag atcttaagcc 54 0
gccn                                     544
```

&lt;210&gt; 455

&lt;211&gt; 344

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(344)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(344)

&lt;223&gt; protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)

&lt;400&gt; 455

```
actgcggtga gagccagcgg ccagcgccac cncaacagcc gccagaagna cacgaggaac 60
cggcggcggc gngtgcgngt agggccgtg n gcggtgncgg cgcgggagga gccggannca 120
gccggcnngg gcggngggca ncanggacga gaaggngnnc accaaggagc tggaccagn 180
gaacgagcag cngaacgagn gcaagcagcn gnccgagncc caggncaga gccncagcga 240
gaangcnaaa gaaanccnga caaaagaanc caacngcaa gaggnncgan gnccaggnac 30 0
ngnccngnga gangngcang ggcaannnca ngaacccatg gaac                                     344
```

&lt;210&gt; 456

&lt;211&gt; 514

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(514)

&lt;223&gt; 5' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(514)  
<223> S100 calcium-binding protein A11 (calgizzarin)  
(S100A11)

<400> 456  
cagcctcccc cgctcgctc agctccaaca tggcaaaaat ctccagccct acagagactg 60  
agcgggtgcat cgagtccttg attgctgtct tccagaagta tgctggaa ag gatggttata 120  
actacactct ctccaagaca gagttcctaa gcttcatgaa tacagaacta gctgccttca 180  
caaagaacca gaaggaccct ggtgtccttg accgcatgat gaagaaactg gacaccaaca 240  
gtgatggtca gctagatttc tcagaatttc ttaatctgat tggtaggcta gctatggctt 300  
gccatggact ccttcctcaa ggctgtccct tcccagaagc gggacctgga gggacccctt 360  
gggccctggg cctttcaaac ccacccctn ttcctttcca gcctttctgt tcatcatntt 420  
ccacagccca cccttncctg gaggcacatt aaccacctna tggtagggtn ccaactggtc 480  
attagttatt aaaggnaatg tnaatttttt ttaa 514

<210> 457  
<211> 359  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(359)  
<223> 5' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(359)  
<223> Granzyme A (granzyme 1, cytotoxic  
T-lymphocyte-associated serine esterase 3) (GZMA)

<400> 457  
gctggacgtc atcaacaagc attcattcaa caacttccgc ctgcgagtg ggtgaacca 60  
tggacccgta gtagctggag ttattggggc ccagaagccg caatatgaca ttgggggcaa 120  
cacagtgaac gtggccagcc gcatggagag tacaggagtc cttggcaaaa tccaagtgaac 180  
tgaggagaca gcatggggccc tacagtcctt gggctacacc tgctacagcc nggggtgtca 240  
tcanggtgaa aggcaaaggg cagctctgca cctacttcct gaacacagac ttgacacgaa 300  
ctggacctcc ttcagctacc ctaggctgag attgcactcg cct tncctaag aacctnaat 359

<210> 458  
<211> 1251  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1251)  
<223> 3' terminal sequence

<220>

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&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1251)

&lt;223&gt; endothelin 1 (EDN1)

&lt;400&gt; 458

```
ggagctgtttt acccccactc taataggggt tcaatataaa aagccggcag agagctgtcc 60
aagtacagacg cgcctctgca tctgcgccag gcgaacgggt cctgcgcctc ctgcagtccc 120
agctctccac caccgcgcg tgcgcctgca gacgctccgc tcgctgcctt ctctcctggc 180
agggcgtgcc ttttctcccc gttaaagggc acttgggctg aaggatcgct ttgagatctg 240
aggaaccgcg agcgctttga gggacctgaa gctgtttttc ttcgttttcc tttgggttca 300
gtttgaacgg gaggtttttg atcccttttt ttcagaatgg attatttgct catgattttc 360
tctctgctgt ttgtggcttg ccaaggagct cc agaaacag cagtcttagg cgctgagctc 420
agcgcggttg gtgagaacgg cggggagaaa cccactccca gtccaccctg ggggctccgc 480
cggccaagc gctgctctg ctgcctcctg atggataaag agtgtgtcta cttctgccac 540
ctggacatca tttgggtcaa cactcccgag cacgttggtc cgtatggact tggaagccct 600
aggtccaaga gagccttgga gaatttactt cccacaaagg caacagaccg tgagaataga 660
tgccaatgtg ctagccaaaa agacaagaag tgctggaatt tttgccaagc aggaaaagaa 720
ctcagggctg aagacattat ggagaaagac tggaataatc ataagaaagg aaaagactgt 780
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agttcagagg aacacctaa acaaaccagg tcggagacca tgagaaacag cgtcaaatca 900
tcttttcatt atccaagct gaaaggcaag ccctccagag agcggttatgt gaccacaac 960
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```

&lt;210&gt; 459

&lt;211&gt; 2145

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2145)

&lt;223&gt; 3' terminal séquence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2145)

<223> Protein tyrosine phosphatase, non -receptor type 6  
(PTPN6)

&lt;400&gt; 459

```
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ccttctctct cggaagcccc caggatggtg aggtggtttc accgagacct cagtgggctg 180
gatgcagaga ccctgctcaa gggccgaggt gtccacggta gcttctctggc tcggccagct 240
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cggatccaga actcagggga tttctatgac ctgtatggag gggagaagt t tgcgactctg 360
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atcatccacc tcaagtacc gctgaactgc tccgatccca ctagttagag gtggtacat 480
ggccacatgt ctggcgggca ggcagagacg ctgctgcagg ccaagggcga gccctggacg 540
tttcttgtgc gtgaga gcct cagccagcct ggagacttcg tgctttctgt gctcagtgc 600
cagcccaagg ctggcccagg ctccccgctc aggggtcacc acatcaaggt catgtgcgag 660
ggtggacgct acacagtggg tggtttggag accttcgaca gcctcacgga cctggtggag 720
```

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```

catttcaaga agacggggat tgaggaggcc tcaggcgccct ttgtctacct gcggcagccg 780
tactatgcc aaggggtgaa tgccgctgac attgagaacc gagtgttgga actgaacaag 840
aagcaggagt ccgaggatac agccaaggct ggcttctggg aggagttga gagtttgag 900
aagcaggagg tgaagaactt gcaccagcgt ctggaagggc aacggccaga gaacaagggc 960
aagaaccgct acaagaa cat tctccccttt gaccacagcc gagtgatcct gcagggacgg 1020
gacagtaaca tccccgggtc cgactacatc aatgccaaact acatcaagaa ccagctgcta 1080
ggccctgatg agaacgctaa gacctacatc gccagccagg gctgtctgga ggccacgggc 1140
aatgacttct ggagatggc gtggcaggag aacagccgtg tcacgtcat gaccacccga 1200
gaggtggaga aaggccggaa caaatgcgtc ccatactggc ccgaggtggg catgcagcgt 1260
gcttatgggc cctactctgt gaccaactgc ggggagcatg acacaaccga atacaaactc 1320
cgtaccttac aggtctcccc gctggacaat ggagacctga ttcgggagat ctggcattac 1380
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tgcagcgccg gcatcgccg cacaggcacc atcattgtca tcgacatgct catggagaac 1560
atctccacca agggcctgga ctgtgacatt gcacatccaga agaccatcca g atggtgagg 1620
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tcccgcacct cgtccaaac a caaggaggat gtgtatgaga acctgcacac taagaacaag 1860
agggaggaga aagtgaagaa gcagcgggtc gcagacaagg agaagagcaa gggttccctc 1920
aagaggaaat gagcggtgct gtccctcagg ggccatgcct cagccctgac cctgtggaag 1980
catttcgcga tggacagact cacaacctga acctaggagt gccccattct tt tgtaattt 2040
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cagggccaac ccttctctc ttgtaaataa agccctggga tcaact 2145

```

&lt;210&gt; 460

&lt;211&gt; 2149

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2149)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2149)

&lt;223&gt; Transcription factor AP -4 (activating enhancer binding protein 4) (TFAP4)

&lt;400&gt; 460

```

gacctgcaaa cacacacac a cacacacaca cacacacaca cacacacaca catacacacg 60
caccagggca gccgagagac ctccctcccg cccctcccat gccgcctcc ctcccctcgc 120
cgccgcccgc gccgccagca tctgggaccg gccgattctg cacctccgtc cggcgtgcc 180
ctttgattcg gatttccatc ttgcattctc cggtgatcg cgggacctgg ct cgtgcaga 240
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ccactaacc cagagactca gcgggaccag gagcggcgga ttcggcgga gatcgccaac 420
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gaaggcatag gctccccgga catctgggag gacgagaagg cggaggacct gcggcgagg 720
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```

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```
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ggagaagcta ttatattttg ttaagaaagt gggggagaaaa aaaaccaaga ggccaccgtg 2100
cctttgtaaa gaaacaaaat aaa gtttgta ctttgttttt taaaaaaaaa 2149
```

&lt;210&gt; 461

&lt;211&gt; 6478

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(6478)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(6478)

&lt;223&gt; Cyclin D2 (CCND2)

&lt;400&gt; 461

```
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cccgaggctc tgctcgccca ccacccaatc ctgcctccc ttctgctcca ccttctctct 120
ctgcctcac ctctcccccg aaaacccctt atttagccaa aggaagg agg tcagggggaa 180
gctctccctt ccccttccaa aaaacaaaaa cagaaaaacc cttttccagg ccggggaag 240
caggagggag aggggcgcgc gggtggcca tggagctgct gtgccacgag gtggaccgg 300
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```

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 ttcccccagc ctgccaatt ttgatcctc ccctctttt gccaaatcct agggggaaga 4740

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```
aatcctagta tgccaaaaat atatgctaag cataattaaa ctccatgcgg gtccata aca 4800
gccaaagaagc ctgcaggaga aagccaaggg cagttccctc cgcagaacac cccatgcgtg 4860
ctgagaggcg agctccttga agaaggggct gttcttccag gaggccttat tttgaactgc 4920
ctcaggaccc cactggagag cacagcatgc cttactactg ggtcatcctt ggtctatgtg 4980
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gttcatgcag ccatccattt gtgcaaaata gggtaagaag attcaagagg atatttatt a 5640
cttctcata ccacatggct tttgatgatt ctggattcta aacaaccag aatggtcatt 5700
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```

&lt;210&gt; 462

&lt;211&gt; 3490

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3490)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3490)

&lt;223&gt; Junction plakoglobin (JUP)

&lt;400&gt; 462

```
cgccagagtc cggagcagcc gcgcgccgac cgcgcgcgagc tcagttcgct gtccgcgccg 60
gtcccaccc cggcccagacc ccgaccgcgc cgggtcaggc cccatactca gtagccacga 120
tgagggtgat gaacctgatg gacgagccta tcaaggtagc tgagtggcag cagacataca 180
cctacgactc gggatatccac tcgggcgcga acacctgcgt gccctccgtc agcagcaagg 240
gcatcatgga ggaggatgag gcctgcgggc gccagtacac gctcaagaaa accaccactt 300
acaccaggg ggtgcccccc agccaagggt acctggagta ccagatgtcc acaacagcca 360
gggcaaacg ggtgcgggag gccatgtgcc ctgggtgtgc ag gcgaggac agctcgcttc 420
tgctggccac ccagggtggag gggcaggcca ccaacctgca gcgactggcc gagccgtccc 480
agctgctcaa gtcggccatt gtgcatctca tcaactacca ggacgatgcc gagctggcca 540
ctcgcgcctt gcccagagtc accaaactgc tcaacgacga ggaccgggtg gtggtgacca 600
```



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aggcgcccat gattgtgaac cagctgtcga agaaggaggc gtcgcgccgg gccctgatgg 660
gctcgcccca gctgggtggcc gctgtcgtgc gtacatgca gaataccagc gacctggaca 720
cagcccgctg caccaccagc atcctgcaca acctctccca ccaccgggag gggctgctcg 780
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cggctcctgtt ctatgccatc accacgctgc acaacctgct cctgtaccag gaggcgcca 900
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tgaccagcaa cagccccgcg ctggtgcaga actgctgtg gacc ctgcgc aacctctcag 1260
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gtgtggatga cgtcaacgtc ctacacctgt ccacgggac actctccaac ctgacatgca 1380
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ccatcctcgt tgcctgtgac aaggacgaca tcacggagcc tgcgctctgc gctctgcgcc 1500
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cagcggtcat ccccgctc gtccaactgc tggtaaggc ccaccaggat gccagcgcc 1740
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ctgccacctc cgtgctgcc gtctgttcc gcatctccga ggacaa gaac ccagactacc 2100
ggaagcgct gtccgtggag ctacccaact cctcttcaa gcatgaccg gctgcctggg 2160
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atggagacta cccatcgac acctacagc agcgctcag gccccgtac cccactgcag 2340
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tcctctctag aacctccttc tgttgaggc cctccatct ccccgctgaa acctgcgctc 2460
cttttttggg gggatccttt gctgctgagc ttccccaagc acggtgt gcc ctggcctgcc 2520
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caggcgatgg ggcaagacag aaaagtgcct gagctgggga agccggggtg taacttcctg 2760
ctgcacctg cgcctccaga ggtcctcct aggtctttc ttgggtagt gttctgctcc 2820
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ggtctgattt tctcctgaa ctccaccgac caactgcct aagccccag ggcctccagg 3060
gccaggttc gagacccaaa ccccaaaaat ccaaaaactt tcttgaaaag ttcagggacc 3120
gtccagggga gatggggagg agatatggag tgagtcacct gctccagaag atgccagctt 3180
ctctctccag ggtgcttagt tggctttgcc caccctcac tcccaggga gctccgggga 3240
cagcttctc acaccctgt cccaccaca cagctgcct agctgacccc gagaagtgt 3300
cttggctgac cctctggtg tgtggtgagg ggctttctc tcccttcc t gtttcagacc 3360
ccccatttc cgcacatgg tgtggggggc tgggggagg ccaagcagag tgttttatta 3420
ttatcgcttt atgtttttg ttattggtt ttttgtatg accaaagcaa agaaaataaa 3480
aataacacag                                     3490

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&lt;210&gt; 463

&lt;211&gt; 1355

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

<221> misc\_feature  
<222> (1)..(1355)  
<223> 3' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(1355)  
<223> Growth arrest and DNA -damage-inducible, alpha  
(GADD45A)

<400> 463  
cagtggtgctgg taggcagtggt ctgggaggca gcgggccaat tagtgtcgtg cggcccgtgg 60  
cgaggcgagg tccgggggagc gagcgagcaa gcaaggcggg aggggtggcc ggagctgcgg 120  
cggttgccac aggaggagga gcccgggagg gcgaggggag gccggagagc gccagggcct 180  
gagctgcccgg agcggcgccct gtgagtgaat gcagaaagca ggcggccgag cgctagccgt 240  
ggcaggagca gcccgcacgc cgcgtctctt ccctgggaga cctgcagttt gcaatatgac 300  
tttgaggagaa ttctcggctg gagagcagaa gaccgaaagg atggataagg tgggggatgc 360  
cctggaggagaa gtgctcagca aagccctgag tc agcgcacg atcactgtcg ggggtgtacga 420  
agcggccaag ctgctcaacg tcgaccccca taacgtgggtg ttgtgcctgc tggcggcgga 480  
cgaggacgac gacagagatg ttgctctgca gatccacttc accctgatcc aggcgttttg 540  
ctgcgagaac gacatcaaca tctgcgcgt cagcaaccgg ggcgggctgg cggagctcct 600  
gctcttggag accgacgtg gccccgcggc gagcgagggc gccgagcagc ccccgacact 660  
gcaactgcgtg ctggtgacga atccacattc atctcaatgg aaggatcctg ccttaagtca 720  
acttatttgt ttttgccggg aaagtcgcta catggatcaa tgggttccag tgattaatct 780  
cctgaacgg tgatggcctc tgaatgaaaa taa ctgaacc aaattgcact gaagtttttg 840  
aaataccttt gtagttactc aagcagttac tccctacact gatgcaagga ttacagaaac 900  
tgatgccaag gggctgagtg agttcaacta catgttcttg gggcccgag atagatgact 960  
ttgcagatgg aaagaggtga aaatgaagaa ggaagctgtg ttgaaacaga aaaataagtc 1020  
aaaaggaaaca aaaattacaa agaaccatgc aggaaggaaa actatgtatt aatttagaat 1080  
ggttgagtta cattaataata aaccaaatat gttaaagttt aagtgtgcag ccatagtttg 1140  
ggtatttttg gtttatatgc cctcaagtaa aagaaaagcc gaaagggta atcatatttg 1200  
aaaaccatat tttattgtat tttgatgaga tatt aaattc tcaaagtttt attataaatt 1260  
ctactaagtt attttatgac atgaaaagtt atttatgcta taaatttttt gaaacacaat 1320  
acctacaata aactggtatg aataattgca tcatt 1355

<210> 464  
<211> 732  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(732)  
<223> 3' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(732)  
<223> Non-metastatic cells 1, protein (NM23A) expressed  
in (NME1)

<400> 464  
tgctgcgaac cacgtgggtc cggggcgctg ttccgggtgct ggcggctgca gccggagttc 60  
aaacctaagc agctggaagg aaccatggcc aactgtgagc gtaccttcat tgcgatcaaa 120  
ccagatgggg tccagcgggg tcttgtggga gagattatca agcgttttga gcagaaagga 180  
ttccgccttg ttggtctgaa attcatgcaa gcttccgaag atcttctcaa ggaacactac 240  
gttgacctga aggaccgtcc attctttgcc ggctggtga aatacatgca ctcagggccg 300

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gtagttgccca tgggtctggga ggggctgaat gtgggtgaaga cgggccgagt catgctcggg 360  
 gagaccaacc ctgcagactc caagcctggg accatccgtg gagacttctg catacaagtt 420  
 ggcaggaaca ttatacat gg cagtgattct gtggagagtg cagagaagga gatcggcttg 480  
 tggtttcacc ctgaggaact ggtagattac acgagctgtg ctcagaactg gatctatgaa 540  
 tgacaggagg gcagaccaca ttgcttttca catccatttc cctccttcc catgggcaga 600  
 ggaccaggct gtaggaaatc tagttattta caggaacttc atcataattt g gaggggaagc 660  
 tcttgagct gtgagttctc cctgtacagt gttaccatcc ccgaccatct gattaaaatg 720  
 ctccctccca gc

&lt;210&gt; 465

&lt;211&gt; 942

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(942)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(942)

&lt;223&gt; Ribosomal protein L13 (RPL13) (ex BBC1)

&lt;400&gt; 465

ctttccgctc ggctgttttc ctgcgcagga gccgcagggc cgtaggcagc catggcgccc 60  
 agccggaatg gcatggtctt gaagccccac ttccacaagg actggcagcg gcgcgtggcc 120  
 acgtggttca accagccggc ccgtaagatc cgcagacgta aggcccggca agccaaggcg 180  
 cgccgcatcg ccccgcgccc cgcgctgggt cccatccggc ccacgtgcyg ctgccccacg 240  
 gttcgggtacc acacgaaggt gcgcgcgggc cgcggttca gcctggagga gctcagggtg 300  
 gccggcattc acaagaaggt ggcccggacc atcggcattt ctgtggatcc gaggaggcgg 360  
 aacaagtcca cggagtccct gcagaccaac gtgcagcggc tgaaggagta ccgctccaaa 420  
 ctcatcctct tccccaggaa gccctcggcc cccaagaagg gagacagttc tgctgaagaa 480  
 ctgaaactgg ccacccagct gaccggaccg gtcattgccc tccggaacgt ctataagaag 540  
 gagaaaagct gagtcacac tgaggaagag aagaatttca aagccttcgc tagtctccgt 600  
 atggcccggtg ccaacgcccg gctcttcggc atacgggcaa aaagagccaa ggaagccgca 660  
 gaacaggatg ttgaaaagaa aaaataaagc cctcctgggg acttgggaatc agtcgggcag 720  
 tcatgtggg tctccacgtg gtgtgtttcg tgggaacaac tgggcctggg atggggcttc 780  
 actgctgtga cttcctctg ccaggggatt tggggctttc ttgaaagaca gtccaagccc 840  
 tggataatgc tttactttct gtgttgaagc actgttggtt gtttggttag tgactgatgt 900  
 aaaacggttt tcttgtggg aggttacaga ggctgacttc ag 942

&lt;210&gt; 466

&lt;211&gt; 755

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(755)

&lt;223&gt; 3' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(755)  
<223> vascular endothelial growth factor B (VEGFB)m

<400> 466  
caccatgagc cctctgctcc gccgcctgct gctcgccgca ctcttgacgc tggccccgc 60  
ccaggccccct gtctcccagc ctgatgcccc tggccaccag aggaaagtgg tgatcatggat 120  
agatgtgtat actcgcgcta cctgccagcc ccgggaggtg gtggtgccct tgactgtgga 180  
gctcatgggc accgtggcca aacagctggt gccagctgc gtgactgtgc agcgtgtgg 240  
tggctgctgc cctgacgatg gcctggagtg tgtgccact gggcagcacc aagtccggat 300  
gcagatcctc atgatccggt acccgagcag t cagctgggg gagatgtccc tggaagaaca 360  
cagccagtgt gaatgcagac ctaaaaaaaaa ggacagtgtc gtgaagccag acagggtgc 420  
cactccccac caccgtcccc agccccgttc tgttccgggc tgggactctg cccccggagc 480  
accctcccca gctgacatca cccatccac tccagcccca ggccccctctg cccagctgc 540  
accagcacc accagcgccc tgacccccgg acctgccgc gccgtgccg acgccgcagc 600  
ttcctccgtt gccaaagggc gggttagag ctcaaccag acacctgcag gtgccggaag 660  
ctgcgaaggt gacacatggc ttttcagact cagcaggtg acttgccca gaggtatat 720  
cccagtggg gaacaaagag gagcctgta aa aaa 755

<210> 467  
<211> 1039  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1039)  
<223> 3' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(1039)  
<223> Laminin receptor 1 (67kD, ribosomal protein SA)  
(LAMR1)

<400> 467  
tgccctgtctt ttccgtgcta cctgcagagg ggtccatacg gcgttgttct ggattcccgt 60  
cgtaacttaa agggaaactt tcacaatgtc cggagccctt gatgtcctgc aaatgaagga 120  
ggaggatgtc cttaa gttcc ttgcagcagg aaccactta ggtggcacca atcttgactt 180  
ccagatggaa cagtacatct ataaaaggaa aagtgatggc atctatatca taaatctcaa 240  
gaggacctgg gagaagcttc tgctggcagc tcgtgcaatt gttgccattg aaaaccctgc 300  
tgatgtcagt gttatatcct ccaggaatac tggccagagg gctgtgctg a agtttgctgc 360  
tgccactgga gccactcaa ttgctggcgc cttcactcct ggaaccttca ctaaccagat 420  
ccaggcagcc ttccgggagc caccgcttct tgtggttact gacccaggg ctgaccacca 480  
gcctctcacg gaggcattct atgttaacct acctaccatt gcgtgtgta acacagattc 540  
tcctctgcgc tatgtg gaca ttgccatccc atgcaacaac aaggagctc actcagtggg 600  
tttaatgtgg tggatgctgg ctcggaagt tctgcgcag cgtggcacca tttcccgta 660  
acaccatgg gaggtcatgc ctgatctgta cttctacaga gatcctgaag agattgaaaa 720  
agaagagcag gctgctgctg agaaggcagt gaccaaggag gaatttcagg gtgaatggac 780  
tgctcccgtc cctgagttca ctgctactca gcctgaggtt gcagactggg ctgaaggtgt 840  
acaggtgccc tctgtgccta ttcagcaatt ccctactgaa gactggagcg ctgagcctgc 900  
cacggaagac tggctgcag ctcccactgc tcaggccact gaatgggtag gagcaaccac 960  
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aaaataaaca tcagtttct 1039

<210> 468  
<211> 240  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(240)  
<223> 3' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(240)  
<223> Chorionic somatomammotropin hormone 1 (placental  
lactogen) = LACTOGEN Precursor

<400> 468  
attcggcacg atgactggcc aggggtataaa aagggccac aagagac cgg ctctaggatc 60  
ccaaggccca actccccgaa ccactcaggg tcctgtggca gctcacctag tggcaatggc 120  
tccaggtcc cggaacgtcc ctgactctgg nttttgncct nctctnactg ccctggnttn 180  
aanaagctng tgccttccaa ancgttcgt tatccagggt ttttgaccac gctatgctnc 240

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